



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 184070

TO: Manjunath N Rao
Location: REM-2A01/2C70
Art Unit: 1652
Monday, April 17, 2006
Case Serial Number: 10/784592

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518 *BOB*

barbara.obryen@uspto.gov

Search Notes

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STIC-Biotech/ChemLib*184070*

From: Rao, Manjunath N.
Sent: Tuesday, April 04, 2006 9:46 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search request for 10/784592

From: Manjunath N. Rao
Art Unit 1652, Room 2A01
Mail Box in Room 2C70
Phone: 272-0939

Date: 4-4-06

Please search the following as soon as possible for application with serial number
10/784592

1. **SEQ ID NO: 18 and nucleotides 124-744 of SEQ ID NO:18, against all commercial nucleic acid sequence databases, issued patents/published applications nucleic acid sequence database and pending application nucleic acid sequence database. Please provide a print of results**
2. **SEQ ID NO: 43 and amino acids 42-248 of SEQ ID NO:43 against all commercial amino acid sequence databases, issued patents/published applications amino acid sequence database and pending application amino acid sequence database. Please provide a print of results.**

If you have any questions please call me at the above phone number.

Thanks

4/4/2006

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 12, 2006, 06:55:51 ; Search time 3612 Seconds
(without alignments)
9772.919 Million cell updates/sec

Title: US-10-784-592-18_COPY_124_744
Perfect score: 621
Sequence: 1 aacacgtgtatgattcg.....aaacgacgtatgcttcttcg 621

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 621 | 100.0 | 744 | 6 CS130878 | CS130878 Sequence |
| 2 | 40.8 | 6.6 | 110000 | 1 BA000004 | Continuation (32 o |
| 3 | 40.2 | 6.5 | 239687 | 14 CR932017 | CR932017 Danio rer |
| 4 | 39.8 | 6.4 | 200322 | 14 AC164371 | AC164371 Bos tauru |
| 5 | 39.4 | 6.3 | 204839 | 14 AC144882 | AC144882 Gorilla g |
| 6 | 38.6 | 6.2 | 110000 | 2 AC116984_2 | Continuation (3 of |
| 7 | 38.6 | 6.2 | 110000 | 2 AC116984_3 | Continuation (4 of |
| 8 | 38.6 | 6.2 | 244259 | 14 AC123226 | AC123226 Rattus no |
| 9 | 38.6 | 6.2 | 257204 | 14 AC109987 | AC109987 Rattus no |
| 10 | 38.2 | 6.2 | 116374 | 5 BX571959 | BX571959 Zebrafish |
| 11 | 38.2 | 6.2 | 242081 | 14 CR933779 | CR933779 Danio rer |
| 12 | 37.8 | 6.1 | 576 | 15 AF225410 | AF225410 Gastrodia |
| 13 | 37.8 | 6.1 | 1554 | 15 AY032588 | AY032588 Gastrodia |
| 14 | 37.8 | 6.1 | 173237 | 14 AC155465 | AC155465 Zea mays |
| 15 | 37.8 | 6.1 | 181924 | 14 AC155611 | AC155611 Zea mays |
| 16 | 37.8 | 6.1 | 200412 | 14 AC115666 | AC115666 Rattus no |
| 17 | 37.8 | 6.1 | 279242 | 14 AC114079 | AC114079 Rattus no |
| 18 | 37.8 | 6.1 | 346208 | 14 AC128290 | AC128290 Rattus no |

| | | | | | | | |
|---|----|------|-----|--------|----|-----------|--------------------|
| c | 19 | 37.4 | 6.0 | 2000 | 6 | AX655393 | Sequence |
| | 20 | 37 | 6.0 | 39961 | 8 | AC000044 | Homo sapi |
| | 21 | 37 | 6.0 | 43738 | 8 | AC000034 | Homo sapi |
| c | 22 | 36.6 | 5.9 | 2286 | 15 | LEU78526 | U78526 Lycopersico |
| | 23 | 36.4 | 5.9 | 176422 | 9 | AC158170 | Mus muscu |
| | 24 | 36.2 | 5.8 | 387 | 15 | AF123309 | Gastrodia |
| | 25 | 36.2 | 5.8 | 516 | 15 | GEL277784 | Gastrodia |
| | 26 | 36.2 | 5.8 | 687 | 15 | GEL277785 | Gastrodia |
| | 27 | 36.2 | 5.8 | 687 | 15 | GEL277786 | Gastrodia |
| | 28 | 36.2 | 5.8 | 699 | 15 | GEL277783 | Gastrodia |
| | 29 | 36.2 | 5.8 | 2306 | 15 | AF334813 | Gastrodia |
| | 30 | 36.2 | 5.8 | 110000 | 15 | AP008217 | Continuation (238 |
| | 31 | 36.2 | 5.8 | 149697 | 15 | AC109832 | Oryza sat |
| | 32 | 36.2 | 5.8 | 180695 | 14 | AC109832 | Pan trogl |
| | 33 | 36 | 5.8 | 63331 | 14 | AC140661 | AC084345 Homo sapi |
| c | 34 | 36 | 5.8 | 216589 | 14 | AC084345 | Homo sapi |
| c | 35 | 35.6 | 5.7 | 26557 | 8 | DQ001128 | AC091741 Homo sapi |
| c | 36 | 35.6 | 5.7 | 79438 | 8 | HSDJ547C9 | DQ001128 Homo sapi |
| c | 37 | 35.6 | 5.7 | 134953 | 14 | AC026088 | AL109927 Human DNA |
| | 38 | 35.6 | 5.7 | 154350 | 8 | AC016948 | AC026088 Homo sapi |
| | 39 | 35.6 | 5.7 | 194418 | 5 | EX001055 | AC016948 Homo sapi |
| c | 40 | 35.6 | 5.7 | 197196 | 14 | AC112585 | BX001055 Zebrafish |
| c | 41 | 35.6 | 5.7 | 254684 | 14 | AC094805 | AC112585 Rattus no |
| c | 42 | 35.2 | 5.7 | 482 | 15 | AF472209 | AC094805 Rattus no |
| c | 43 | 35.2 | 5.7 | 482 | 15 | AF472211 | AF472209 Arabidops |
| c | 44 | 35.2 | 5.7 | 482 | 15 | AF472212 | AF472211 Arabidops |
| c | 45 | 35.2 | 5.7 | 482 | 15 | AF472213 | AF472212 Arabidops |

ALIGNMENTS

RESULT 1 CS130878 Sequence 18 from Patent WO2005066339. 744 bp DNA linear PAT 02-AUG-2005
LOCUS CS130878
DEFINITION CS130878
ACCESSION CS130878
VERSION CS130878.1 GI:71793146
KEYWORDS Alicyclobacillus sp.
SOURCE Alicyclobacillus sp.
ORGANISM Alicyclobacillus sp.
Bacteria; Firmicutes; Bacillales; Alicyclobacillaceae;
Alicyclobacillus.

REFERENCE 1 Wilting, R.
AUTHORS Polypeptides of Alicyclobacillus sp
TITLE Patent: WO 2005066339-A 18 21-JUL-2005;
JOURNAL Novozymes A/S (DK)
FEATURES Location/Qualifiers

source 1..744
/organism="Alicyclobacillus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:61169"
misc_feature 1..744
/note="CDS"
misc_feature 1..123
/notes="sig_peptide"
misc_feature 124..744
/note="mat_peptide"

ORIGIN

Query Match 100.0%; Score 621; DB 6; Length 744;
Best Local Similarity 100.0%; Pred. No. 1.2e-183;
Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACACGGTGTATGATTCGAGGAACACACCGCGGACGCATCAACGGTAAGCGGTACA 60
DB 124 AACACGGTGTATGATTCGAGGAACACACCGCGGACGCATCAACGGTAAGCGGTACA 183
QY 61 ACTTCTTTGGTTAATTCGACGAATAGTTTCACAGGTAGCAAGCAAGCAAACTCCAGT 120
DB 184 ACTTCTTTGGTTAATTCGACGAATAGTTTCACAGGTAGCAAGCAAGCAAACTCCAGT 243

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QY 121 ACGTCTCCGCTCATAGTCTACGAACTCAATTGCAACATGCGCAACATCAAGTGTCTACG 180
Db 244 ACGTCTCCGCTCATAGTCTACGAACTCAATTGCAACATGCGCAACATCAAGTGTCTACG 303
QY 181 ACTTCATCTCTCAGTCGAAGTTACGATATATCCGTTTTCACACATACGGGAAGGTAGGA 240
Db 304 ACTTCATCTCTCAGTCGAAGTTACGATATATCCGTTTTCACACATACGGGAAGGTAGGA 363
QY 241 GACTTGAATAATTAGATTAACTCCCTGCGCAAGTTAAAGAGTGTGGGGTACGACGGGATA 300
Db 364 GACTTGAATAATTAGATTAACTCCCTGCGCAAGTTAAAGAGTGTGGGGTACGACGGGATA 423
QY 301 GGTGAACCCGAAATGTCGTTTGGGTTTATCAACATCACCAATAGAAATGACGGATCC 360
Db 424 GGTGAACCCGAAATGTCGTTTGGGTTTATCAACATCACCAATAGAAATGACGGATCC 483
QY 361 ACTCCTATGAGGTCGTTGATGCAATATTCATTTGCGAATCTTAACGGGAAGGTTTAT 420
Db 484 ACTCCTATGAGGTCGTTGATGCAATATTCATTTGCGAATCTTAACGGGAAGGTTTAT 543
QY 421 CAGCCGATTTCTACTGCTGAGATATATGCAAAATCAAAATTCAGGACTATTCGACCGAC 480
Db 544 CAGCCGATTTCTACTGCTGAGATATATGCAAAATCAAAATTCAGGACTATTCGACCGAC 603
QY 481 CTCAACCTGTCGTCATGACGACAAATCTCGTATTTGATATGCGGATTTTATGACA 540
Db 604 CTCAACCTGTCGTCATGACGACAAATCTCGTATTTGATATGCGGATTTTATGACA 663
QY 541 TATGTCACGTCGGGAGCATTTACTCATTTGTCCTTCCATGGTTCCTTCGGGTCAGAT 600
Db 664 TATGTCACGTCGGGAGCATTTACTCATTTGTCCTTCCATGGTTCCTTCGGGTCAGAT 723
QY 601 GAAACGACGTATGCTCTTCGG 621
Db 724 GAAACGACGTATGCTCTTCGG 744

RESULT 2
BA000004_31/c
WPCOMMENT
Sequence split into 42 fragments LOCUS BA000004 Accession BA000004
Fragment Name Begin End
BA000004_00 1 110000
BA000004_01 100001 210000
BA000004_02 200001 310000
BA000004_03 300001 410000
BA000004_04 400001 510000
BA000004_05 500001 610000
BA000004_06 600001 710000
BA000004_07 700001 810000
BA000004_08 800001 910000
BA000004_09 900001 1010000
BA000004_10 1000001 1110000
BA000004_11 1100001 1210000
BA000004_12 1200001 1310000
BA000004_13 1300001 1410000
BA000004_14 1400001 1510000
BA000004_15 1500001 1610000
BA000004_16 1600001 1710000
BA000004_17 1700001 1810000
BA000004_18 1800001 1910000
BA000004_19 1900001 2010000
BA000004_20 2000001 2110000
BA000004_21 2100001 2210000
BA000004_22 2200001 2310000
BA000004_23 2300001 2410000
BA000004_24 2400001 2510000
BA000004_25 2500001 2610000
BA000004_26 2600001 2710000
BA000004_27 2700001 2810000
BA000004_28 2800001 2910000
BA000004_29 2900001 3010000
BA000004_30 3000001 3110000
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BA000004_31 3100001 3210000
BA000004_32 3200001 3310000
BA000004_33 3300001 3410000
BA000004_34 3400001 3510000
BA000004_35 3500001 3610000
BA000004_36 3600001 3710000
BA000004_37 3700001 3810000
BA000004_38 3800001 3910000
BA000004_39 3900001 4010000
BA000004_40 4000001 4110000
BA000004_41 4100001 4202352
Continuation (32 of 42) of BA000004 from base 3100001 (BA000004 Bacillus halodurans C-12)

Query Match 6.6%; Score 40.8; DB 1; Length 110000;
Best Local Similarity 51.8%; Pred. No. 0.49;
Matches 118; Conservative 0; Mismatches 107; Indels 3; Gaps 1;

QY 303 TGAACCGGAAATGTCGTTTGGGTTTATCAACATCACCAATAGAAATGACGGATCCAC 362
Db 87150 TGCAGAGCGGAAAGGAACTTTCCTTATTTGATGTAAACAATCAAAAATGAAGGAGCGA 87091
QY 363 TCCATGAGGTCGTTGATGCGCATATTCATTTGCAGAACTTAAACGGGAACGTTTATCA 422
Db 87090 CTCATTTACGTTGATTCGTCCTTTCTTAATTAAGTCGGAGATG---TAGAATATGA 87034
QY 423 GCCGGATTTCTACTGCTGAGATATATGCAATACAAATTCAGGAGCACTATTCGACCGACCT 482
Db 87033 TTCGATTCCTCTGCTGGACTTTACGGGATGAAGTGTCTGACTTTTCTCTACTAGCT 86974
QY 483 CAACCTGTCGTCATGACGACAAATCTCGTATTTGATATGCCGGA 530
Db 86973 AAATCCTGTTTGGAACTACCGGTAAGTGTATTTGATGTTTCCGCA 86926

RESULT 3
CR932017 239687 bp DNA linear HTG 22-MAY-2005
LOCUS
DEFINITION
Danio rerio clone DKEY-33F9, WORKING DRAFT SEQUENCE, 7 unordered
pieces.
ACCESSION
CR932017
VERSION
CR932017.4 GI:66392865
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 239687)
AUTHORS
McLaren,S.
TITLE
Direct Submission
JOURNAL
Submitted (21-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfsh-help@sanger.ac.uk Clone requests: clonereques@sanger.ac.uk
On May 22, 2005 this sequence version replaced gi:56797647.
COMMENT
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfsh-help@sanger.ac.uk
----- Project Information
Center project name: zK33F9
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 235298 bases at least Q40
Consensus quality: 235832 bases at least Q30
Consensus quality: 236380 bases at least Q20
Insert size: 239087; sum-of-contigs
Insert size: 217257; 9.8% error; agarose-fp
Quality coverage: 9.53x in Q20 bases; sum-of-contigs Quality
coverage: 10.66x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
```


(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Project name: FHSB
Center project name: FHSB
Center clone name: CH240-11714

----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 190643 bases at least Q40
Consensus quality: 193630 bases at least Q30
Consensus quality: 195478 bases at least Q20

Estimated insert size: 198954; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 5877: contig of 5877 bp in length
* 5878 6322: gap of 445 bp
* 6323 18172: contig of 11850 bp in length
* 18173 18222: gap of 50 bp
* 18223 20528: contig of 2304 bp in length
* 20527 20576: gap of 50 bp
* 20577 35742: contig of 15166 bp in length
* 35743 36222: gap of 480 bp
* 36223 38281: contig of 2059 bp in length
* 38282 38381: gap of unknown length
* 38382 41148: contig of 2766 bp in length
* 41148 41197: gap of 50 bp
* 41198 55437: contig of 14240 bp in length
* 55438 55562: gap of 125 bp
* 55563 86280: contig of 30718 bp in length
* 86281 86330: gap of 50 bp
* 86331 92028: contig of 5698 bp in length
* 92029 92078: gap of 50 bp
* 92079 119970: contig of 27892 bp in length
* 119971 120047: gap of 77 bp
* 120048 123375: contig of 3328 bp in length
* 123376 123665: gap of 290 bp
* 123666 142980: contig of 19315 bp in length
* 142981 143080: gap of unknown length
* 143081 144260: contig of 1180 bp in length
* 144261 145079: gap of 819 bp
* 145080 192359: contig of 47280 bp in length
* 192360 192458: gap of unknown length
* 192459 193549: contig of 1090 bp in length
* 193550 193649: gap of unknown length
* 193650 195025: contig of 1376 bp in length
* 195026 195125: gap of unknown length
* 195126 196204: contig of 1079 bp in length
* 196205 196304: gap of unknown length
* 196305 197805: contig of 1501 bp in length
* 197806 197905: gap of unknown length
* 197906 200322: contig of 2417 bp in length.

FEATURES

| source | Location/Qualifiers |
|-----------------------|---|
| 1. .200322 | /organism="Bos taurus" |
| | /mol_type="genomic DNA" |
| | /db_xref="taxon:9913" |
| | /clone="CH240-11714" |
| 5878. .6322 | /estimated_length=445 |
| 18173. .18222 | /estimated_length=50 |
| 20527. .20576 | /estimated_length=50 |
| 35743. .36222 | /estimated_length=480 |
| 38282. .38381 | /estimated_length=unknown |
| 41148. .41197 | /estimated_length=50 |
| 55438. .55562 | /estimated_length=125 |
| 86281. .86330 | /estimated_length=50 |
| 92029. .92078 | /estimated_length=50 |
| 119971. .120047 | /estimated_length=77 |
| 123376. .123665 | /estimated_length=290 |
| 142981. .143080 | /estimated_length=unknown |
| 144261. .145079 | /estimated_length=819 |
| 192360. .192459 | /estimated_length=unknown |
| 193550. .193649 | /estimated_length=unknown |
| 195026. .195125 | /estimated_length=unknown |
| 196205. .196304 | /estimated_length=unknown |
| 197806. .197905 | /estimated_length=unknown |
| ORIGIN | |
| Query Match | 6.4%; Score 39.8; DB 14; Length 200322; |
| Best Local Similarity | 60.7%; Pred.No.1; |
| Matches | 65; Conservative 0; Mismatches 42; Indels 0; Gaps 0; |
| Qy | 199 AAGTTACGATATATCCCGTTTCACATACGGAAGTAGGAGACTTTGGAAATTAGATT 258 |
| Db | 13752 AGGTGACACATGCGACAGTCTTCTCTCCGGAAGTAGGAGCTCTCTGGAGATTAGAGGA 13811 |
| Qy | 259 AACTCCCTGCGACGAGTTAAGAGTGTGGGTACGACGGGATAGGTGA 305 |
| Db | 13812 AAAACCTCTGTAGATACAAATCTGGGCTCTCGGGGAAGGGGA 13858 |
| RESULT 5 | |
| AC144882 | 204839 bp DNA linear HTG 18-JUN-2003 |
| LOCUS | Gorilla gorilla gorilla clone CH255-154N17, WORKING DRAFT SEQUENCE, |
| DEFINITION | 2 ordered pieces. |
| AC144882 | AC144882.2 GI:31880084 |
| VERSION | HTG; HTGS PHASE2; HTGS DRAFT. |
| KEYWORDS | Gorilla gorilla gorilla (lowland gorilla) |
| SOURCE | Gorilla gorilla gorilla |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Gorilla |
| REFERENCE | 1 (bases 1 to 204839) |
| AUTHORS | Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Cariaga,K., |

Chu, G., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurlb, B., Idol, J.R., Karling, E., Kwong, P., Laric, P., Lee-Lin, S.-Q., Legaapi, R., Maduro, Q.L., Maguiv, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Padgett, A.B., Pearson, R., Portnoy, M.B., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantiripos, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.

NISC Comparative Sequencing Initiative

Unpublished

2 (bases 1 to 204839)

Green, E.D.

Direct Submission

Submitted (23-MAY-2003) NIH Intramural Sequencing Center, 8717 Grommont Circle, Gaithersburg, MD 20877, USA

3 (bases 1 to 204839)

Green, E.D.

Direct Submission

Submitted (18-JUN-2003) NIH Intramural Sequencing Center, 8717 Grommont Circle, Gaithersburg, MD 20877, USA

On Jun 18, 2003 this sequence version replaced gi:3104297.

----- Genome Center

Center: NIH Intramural Sequencing Center

Center code: NISC

Web site: <http://www.nisc.nih.gov>

Contact: nisc_zoo@nigri.nih.gov

----- Project Information

Center project name: enf

Center clone name: 154N17

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

Summary statistics

Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.90319
Consensus quality: 204590 bases at least Q40
Consensus quality: 204680 bases at least Q30
Consensus quality: 204709 bases at least Q20
Insert size: 192000; agarose-fp
Insert size: 204739; sum-of-ontigs
Quality coverage: 11.99x in Q20 bases; agarose-fp
Quality coverage: 11.24x in Q20 bases; sum-of-ontigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * been provided by the submittor.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be provided.
 * 1 187431: contig of 187431 bp in length
 * 187432 187531: gap of unknown length
 * 187532 204939: contig of 17308 bp in length.

FEATURES
SOURCE

```

/misc_feature
1. .187431
/clone_lib="CH255"
/notes="assembly_fragment
clone_end:T7
vector_side:left"
misc_feature
1. .15E17
/notes="clone overlaps with GenBank Accession Number
AC144464 clone CH255-473J23 (center project name end)"
187432. .187531
/estimated_length=unknown
187532. .204839
/notes="assembly_fragment
clone_end:SP6
vector_side:right"
ORIGIN
Query Match 6.3%; Score 39.4; DB 14; Length 204839;
Best Local Similarity 52.1%; Pred. No. 1.4;
Matches 88; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
Qy 259 AACTCCCTGCAGCAAGTTAAGAGTGTGGGGTACGACGGGATAGGTGAACCCCAATGGT 318
Db 69349 AGCACAATGCACACAGTTCACAGCAAGGAGGACATGCAATTGCTGTACACCAACCT 69408
Qy 319 GCGTTTGGGTATCAACATCACCATAAGAAATGACGGATCCACTCTTATGAGGTCTGTT 378
Db 69409 GCCTATAGCCTTAGCCACAGCAACATATAAAATGTAATCTTAACCTAATGACGGCTTG 69468
Qy 379 GATGGCATATTCATTTGCAGAACTTAAACGGGAACGTTTATCAGCCGG 427
Db 69469 CTTCTGCCAACCTGATTTAGAAATATAGTGTATATTTCTTCCTGG 69517
RESULT 6
AC116984_2
WPCOMMENT
Sequence split into 6 fragments LOCUS AC116984 Accession AC116984
Fragment Name Begin End
AC116984_0 1 110000
AC116984_1 100001 210000
AC116984_2 200001 310000
AC116984_3 300001 410000
AC116984_4 400001 510000
AC116984_5 500001 541399
Continuation (3 of 6) of AC116984 from base 200001 (AC116984 Dictyostelium discoidi)
Query Match 6.2%; Score 38.6; DB 2; Length 110000;
Best Local Similarity 51.4%; Pred. No. 2.4;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
Qy 299 TAGGTGAACCGCAAAATGGTGCCTTTGGGTTCACACATCACCAATAAGAAATGACGGAT 358
Db 100885 TGGTTGAAAAGAAAATAAAGTAATGATATCAACAAAACCGTATTAGATGCGAT 100944
Qy 359 CCACTCCTATGGAGGTGCTTGATGGCATATTCATTTGCAGAACTTAAACGGGAACGTTT 418
Db 100945 CTTTGTGTAATGATCACCGAGTGGTTTAGCTTACATTAATAATGGGTATTGGTAAAGATG 101004
Qy 419 ATCAGCCGGATTCCTACTGCTGAGATATATGCAATACAAATTCAGGACTATT 471
Db 101005 CAACTTCAATGTTTACTGGTGAAGTTTATGCTCATTCAAATGCTGCTAAAAAT 101057
RESULT 7
AC116984_3
WPCOMMENT
Sequence split into 6 fragments LOCUS AC116984 Accession AC116984
Fragment Name Begin End
AC116984_0 1 110000
AC116984_1 100001 210000
AC116984_2 200001 310000
AC116984_3 300001 410000
AC116984_4 400001 510000

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Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, P.,
Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederstockern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 244259)
Worley, K.C.

Direct Submission
Submitted (29-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 244259)
Rat Genome Sequencing Consortium.

Direct Submission
Submitted (08-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Sep 19, 2002 this sequence version replaced gi:21671648.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GSVF
Center clone name: CH230-217M18
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 174893 bases at least Q40
Consensus quality: 180721 bases at least Q30
Consensus quality: 184098 bases at least Q20
Estimated insert size: 195426; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases, sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

1 131499: contig of 131499 bp in length
131500 131599: gap of unknown length
231487 231586: contig of 99887 bp in length
231487 231587: gap of unknown length
232741 232741: contig of 1155 bp in length
232742 232841: gap of unknown length
232842 234462: contig of 1621 bp in length
234463 234562: gap of unknown length
234563 236227: contig of 1665 bp in length
236228 236327: gap of unknown length

| FEATURES | | Location/Qualifiers | |
|---|--------|--|-------|
| * | 236328 | 237975: contig of 1648 bp in length | |
| * | 237976 | 238075: gap of unknown length | |
| * | 238076 | 241664: contig of 3589 bp in length | |
| * | 241665 | 241764: gap of unknown length | |
| * | 241765 | 244259: contig of 2495 bp in length. | |
| source | | 1..244259 | |
| misc_feature | | /organism="Rattus norvegicus" | |
| | | /mol_type="genomic DNA" | |
| | | /db_xref="taxon:10116" | |
| | | /clone="CH230-217M18" | |
| misc_feature | | 1..1078 | |
| | | /note="wgs contig" | |
| misc_feature | | 33392..34674 | |
| | | /note="wgs contig" | |
| misc_feature | | 81130..82304 | |
| | | /note="wgs contig" | |
| misc_feature | | 93183..94437 | |
| | | /note="wgs contig" | |
| gap | | 131500..131599 | |
| | | /estimated_length=unknown | |
| misc_feature | | 199589..201827 | |
| | | /note="wgs contig" | |
| gap | | 231487..231586 | |
| | | /estimated_length=unknown | |
| gap | | 232742..232841 | |
| | | /estimated_length=unknown | |
| gap | | 234463..234562 | |
| | | /estimated_length=unknown | |
| gap | | 236228..236327 | |
| | | /estimated_length=unknown | |
| gap | | 237976..238075 | |
| | | /estimated_length=unknown | |
| gap | | 241665..241764 | |
| | | /estimated_length=unknown | |
| ORIGIN | | | |
| Query Match 6.2%; Score 38.6; DB 14; Length 244259; | | | |
| Best Local Similarity 54.6%; Pred. No. 2.5; | | | |
| Matches 77; Conservative 0; Mismatches 64; Indels 0; Gaps 0; | | | |
| QY | 381 | TGCGCATATTCATTTTCGACGACTTAACGGGACGTTTATCATCGCGGATCTTACTGCTGA | 440 |
| Db | 96563 | TGCGCATCTCGAATTCGACGCCCTTATATGAAGAGTAGCCATCTGAACCTTACTCCTTA | 96504 |
| QY | 441 | GATATATGCAATFACAAATTCAGGGACTATTCGACCGACCTCAACCTGGTGTGTCAT | 500 |
| Db | 96503 | CATTTTTCAGAGGCCATTCATACACTGAGCCATCACCACACCCCATATGTGTAAAT | 96444 |
| QY | 501 | GACGACAAATCTCGTATTGA | 521 |
| Db | 96443 | AGTTCTAAGACCTACATTGA | 96423 |
| RESULT 9 | | | |
| AC109987 | | | |
| LOCUS | | | |
| DEFINITION Rattus norvegicus clone CH230-230B23, *** SEQUENCING IN PROGRESS | | | |
| ***, 13 unordered pieces. | | | |
| AC109987 | | | |
| AC109987.4 GI:23820637 | | | |
| VERSION HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED. | | | |
| KEYWORDS Rattus norvegicus (Norway draft) | | | |
| SOURCE | | | |
| ORGANISM | | | |
| Rattus norvegicus | | | |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; | | | |
| Sciurognathi; Muroidae; Murinae; Rattus. | | | |
| 1 (bases 1 to 257204) | | | |
| REFERENCE | | | |
| AUTHORS Muzny, D. Marie., Metzker, M. Lee., Abranzen, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyatebech, V., Ayodeji, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Muzny, D. Marie., Metzker, M. Lee., Abranzen, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyatebech, V., Ayodeji, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., | | | |

variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see

http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-4616 is from a Zebrafish BAC library

VECTOR: pindigobac-5.

FEATURES

```

source
1. .116374
   Location/Qualifiers
     /organism="Danio rerio"
     /mol_type="genomic DNA"
     /db_xref="taxon:7955"
     /clone="DKEY-4616"
     /clone_lib="DanioKey"

```

ORIGIN

```

Query Match      6.2%; Score 38.2; DB 5; Length 116374;
Best Local Similarity 59.8%; Pred. No. 3.2;
Matches 64; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 385 ATATTCATTTGCAGAACTTAAACGGAACTTTATCAGCGGATTTACTGCTGATGA 444
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 47200 ATATTCAAATTAGTTCTTAGCAGGAATTTACTAACAGATATTAAAGTTTGATATA 47141
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 445 TATGCAATCAAAATTCAGGACTATTCGACGACCTCAACCTCG 491
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 47140 TTTCTGTAGAAATTCACAGATATTTTCATAGAACTCAACCTTG 47094
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```

```

RESULT 11
CR933779/c      242081 bp   DNA   linear   HTG 10-JUN-2005
LOCUS          Danio rerio chromosome 12 clone DKEY-13J5, WORKING DRAFT SEQUENCE,
DEFINITION     12 unordered pieces.
ACCESSION      CR933779
VERSION        CR933779.4 GI:67509338
KEYWORDS       HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
SOURCE         Danio rerio (zebrafish)
ORGANISM       Danio rerio

```

```

REFERENCE
AUTHORS       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
               Cypriniformes; Cyprinidae; Danio.
TITLE          1 (bases 1 to 242081)
JOURNAL        Direct Submission

```

```

SUBMITTED (08-JUN-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests:
http://www.sanger.ac.uk/Projects/D_rerio/faqs.shtml#dataeight
On Jun 10, 2005 this sequence version replaced gi:58330714.

```

COMMENT

```

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC

```

```

Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: zk13J5
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 236648 bases at least Q40
Consensus quality: 237713 bases at least Q30
Consensus quality: 238743 bases at least Q20
Insert size: 240981; sum-of-contigs
Insert size: 168181; 37.4% error; agarose-fp
Quality coverage: 6.79x in Q20 bases; sum-of-contigs Quality
coverage: 9.84x in Q20 bases; agarose-fp
-----

```

```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

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* 1
* 3578: contig of 3578 bp in length
* 3579: gap of 100 bp
* 3679: contig of 10008 bp in length
* 13686: gap of 100 bp
* 13787: contig of 31721 bp in length
* 45507: gap of 100 bp
* 45508: contig of 14827 bp in length
* 60434: gap of 100 bp
* 60435: contig of 11812 bp in length
* 72346: gap of 100 bp
* 72347: contig of 6602 bp in length
* 72447: gap of 100 bp
* 79049: contig of 11130 bp in length
* 79149: gap of 100 bp
* 90279: contig of 41168 bp in length
* 90379: gap of 100 bp
* 131546: contig of 9965 bp in length
* 131647: gap of 100 bp
* 141612: contig of 32173 bp in length
* 141712: gap of 100 bp
* 173885: contig of 63746 bp in length
* 173985: gap of 100 bp
* 237731: contig of 4251 bp in length.
* 237831: Location/Qualifiers

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FEATURES

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   /mol_type="genomic DNA"
   /db_xref="taxon:7955"
   /chromosome="12"
   /clone="DKEY-13J5"
   /clone_lib="DanioKey"
   1. .3578
     /note="assembly fragment:01599"
     fragment_chain:1
     3679. .13686
     /note="assembly fragment:01661"
     fragment_chain:1
     13787. .45507
     /note="assembly fragment:02271"
     fragment_chain:1
     45608. .50434
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     60535. .72346
     /note="assembly fragment:01984"
     fragment_chain:1
     72447. .79048
     /note="assembly fragment:01793"
     fragment_chain:1
     79149. .90278

```

misc_feature

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1. .3578
   /note="assembly fragment:01599"
   fragment_chain:1
   3679. .13686
   /note="assembly fragment:01661"
   fragment_chain:1

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misc_feature

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13787. .45507
   /note="assembly fragment:02271"
   fragment_chain:1
   45608. .50434
   /note="assembly fragment:02110"
   fragment_chain:1

```

misc_feature

```

60535. .72346
   /note="assembly fragment:01984"
   fragment_chain:1
   72447. .79048
   /note="assembly fragment:01793"
   fragment_chain:1

```

misc_feature

```

79149. .90278
   /note="assembly fragment:01793"
   fragment_chain:1

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misc_feature

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79149. .90278
   /note="assembly fragment:01793"
   fragment_chain:1

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misc_feature

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79149. .90278
   /note="assembly fragment:01793"
   fragment_chain:1

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/notes="assembly_fragment:01867
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90379..131546
/notes="assembly_fragment:00001
fragment_chain:1"
131647..141611
/notes="assembly_fragment:01720
fragment_chain:2"
141712..173884
/notes="assembly_fragment:00406
fragment_chain:2"
173985..237730
/notes="assembly_fragment:00838.0"
237831..242081
/notes="assembly_fragment:01615"

ORIGIN
Query Match      6.2%; Score 38.2; DB 14; Length 242081;
Best Local Similarity 59.8%; Pred. No. 3.3;
Matches 64; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 385 ATATTCATTTGCGAAGCTTAACGGGAAGCTTTATCAGCGGAGTTCTACTGCTGAGATA 444
Db 220878 ATATTCGAAATTTAGTTCTTAGCAAGGAAATTTACTAACGAGATATTAAAGTTTGTATATA 220819

Qy 445 TATGCAATACAAATTCAGGAGCTATTCCGACGACCTCAACCTGG 491
Db 220818 TTTTCTGTTAGAAATTCACAGATATTTTCATGAAGTCAACCTTTG 220772

RESULT 12
LOCUS AF225410 576 bp mRNA linear PLN 21-JUL-2005
DEFINITION Gastrodia elata antifungal protein precursor, mRNA, complete cds.
ACCESSION AF225410
VERSION AF225410.2 GI:71040863
KEYWORDS
SOURCE
ORGANISM
Gastrodia elata
Gastrodia elata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
Epilobioideae; lower Epilobioideae; Gastrodiaeae; Gastrodia.
REFERENCE 1 (bases 1 to 576)
AUTHORS Wang, Y., Li, W., and Guo, S.
TITLE Purification, in Vitro Activity and cDNA Cloning of Gastrodia
Antifungal Protein (GAPP) from Gastrodia (Gastrodia elata)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 576)
AUTHORS Wang, Y., Li, W., Fu, R., Guo, S. and Sun, Y.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-2000) Genetics, Institute of Genetics, Datun
Road, Beijing 100101, China
REFERENCE 3 (bases 1 to 576)
AUTHORS Wang, Y., Li, W., Fu, R., Guo, S. and Sun, Y.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2005) Genetics, Institute of Genetics, Datun
Road, Beijing 100101, China
REMARK Sequence update by submitter
COMMENT On Jul 20, 2005 this sequence version replaced gi:12330253.
FEATURES
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/mol_type="mRNA"
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/tissue_type="secondary corn"
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/protein_id="AAGS2664.2"
/db_xref="GI:71040864"
/translaton="MAASASTAVILFFAVTTMMSLSAIPAPASRLNSGHQLDTGGSL
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fragment_chain:1"
90379..131546
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fragment_chain:1"
131647..141611
/notes="assembly_fragment:01720
fragment_chain:2"
141712..173884
/notes="assembly_fragment:00406
fragment_chain:2"
173985..237730
/notes="assembly_fragment:00838.0"
237831..242081
/notes="assembly_fragment:01615"

ORIGIN
Query Match      6.2%; Score 38.2; DB 14; Length 242081;
Best Local Similarity 59.8%; Pred. No. 3.3;
Matches 64; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 385 ATATTCATTTGCGAAGCTTAACGGGAAGCTTTATCAGCGGAGTTCTACTGCTGAGATA 444
Db 220878 ATATTCGAAATTTAGTTCTTAGCAAGGAAATTTACTAACGAGATATTAAAGTTTGTATATA 220819

Qy 445 TATGCAATACAAATTCAGGAGCTATTCCGACGACCTCAACCTGG 491
Db 220818 TTTTCTGTTAGAAATTCACAGATATTTTCATGAAGTCAACCTTTG 220772

RESULT 12
LOCUS AF225410 576 bp mRNA linear PLN 21-JUL-2005
DEFINITION Gastrodia elata antifungal protein precursor, mRNA, complete cds.
ACCESSION AF225410
VERSION AF225410.2 GI:71040863
KEYWORDS
SOURCE
ORGANISM
Gastrodia elata
Gastrodia elata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
Epilobioideae; lower Epilobioideae; Gastrodiaeae; Gastrodia.
REFERENCE 1 (bases 1 to 576)
AUTHORS Wang, Y., Li, W., and Guo, S.
TITLE Purification, in Vitro Activity and cDNA Cloning of Gastrodia
Antifungal Protein (GAPP) from Gastrodia (Gastrodia elata)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 576)
AUTHORS Wang, Y., Li, W., Fu, R., Guo, S. and Sun, Y.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-2000) Genetics, Institute of Genetics, Datun
Road, Beijing 100101, China
REFERENCE 3 (bases 1 to 576)
AUTHORS Wang, Y., Li, W., Fu, R., Guo, S. and Sun, Y.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2005) Genetics, Institute of Genetics, Datun
Road, Beijing 100101, China
REMARK Sequence update by submitter
COMMENT On Jul 20, 2005 this sequence version replaced gi:12330253.
FEATURES
source
1..576
/organism="Gastrodia elata"
/mol_type="mRNA"
/db_xref="taxon:91201"
/tissue_type="secondary corn"
1..540
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/product="antifungal protein precursor"
/protein_id="AAGS2664.2"
/db_xref="GI:71040864"
/translaton="MAASASTAVILFFAVTTMMSLSAIPAPASRLNSGHQLDTGGSL
AQQGLYIQNDCNLVYDNNRVAWSGTNGKAGCGVLRMQDGNLVYSGSRVIMAS
NTNRQNGNYILLQDRNRVYDNNNAIWATHTNVGNAETAI PHSGNGTAAAGSAAQ

```

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NKVNELYISWYSRKRAG"
1..84
85..537
/product="antifungal protein"

ORIGIN
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Best Local Similarity 58.4%; Pred. No. 3.6;
Matches 66; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 256 GTTAACCTCCCTGCGAGCAAGTTAAGAGTGTGGGTACGACGGGATAGTGAACCGCAAT 315
Db 325 GGTAACCTACTATCTGATCTCTTCAGAGAGATCGTAACGTCGTATATACGATAATTCAT 384

Qy 316 GGTGCGTTTGGGTATCAACATCACCATAAGAAATGACGATCCACTCCCTAT 368
Db 385 AATGCGATTTGGGCAACCCACCAACGTTTGGAAATGCTGAATCACTGCGAT 437

RESULT 13
LOCUS AY032588 1554 bp DNA linear PLN 11-JUN-2001
DEFINITION Gastrodia elata antifungal protein gene, complete cds.
ACCESSION AY032588
VERSION AY032588.1 GI:14346011
KEYWORDS
SOURCE
ORGANISM
Gastrodia elata
Gastrodia elata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
Epilobioideae; lower Epilobioideae; Gastrodiaeae; Gastrodia.
REFERENCE 1 (bases 1 to 1554)
AUTHORS Sa, Q.-L., Wang, Y.-Q., Li, W.-B., Zhang, L.-M., Niu, H.-Y. and
Sun, Y.-R.
TITLE Gastrodia elata antifungal protein gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1554)
AUTHORS Sa, Q.-L., Wang, Y.-Q., Li, W.-B., Zhang, L.-M., Niu, H.-Y. and
Sun, Y.-R.
TITLE Direct Submission
JOURNAL Submitted (15-APR-2001) Group 603, Institute of Genetics, Da Tun
Road, Beijing 100101, People's Republic of China
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1..1554
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/mol_type="genomic DNA"
/db_xref="taxon:91201"
1..581
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<582..>1091
/product="antifungal protein"
582..1091
/codon_start=1
/product="antifungal protein"
/protein_id="AAK5994.1"
/db_xref="GI:14346012"
/translaton="MASPASSAVILFFAVAAKSLAMPALASQNLNAGTGTGTGQSL
AQQPQDFVIONDCNLVYDNNRVAWSGTNGKAGCGVLRMQDGNLVYSGSRVIMAS
NTNRDDNYILLQDRNRVYDSSNNAIWATGTNVGNAALTIPHSNGTAAAGSAAQ
NKVNEYLRP"

ORIGIN
Query Match      6.1%; Score 37.8; DB 15; Length 1554;
Best Local Similarity 58.4%; Pred. No. 3.7;
Matches 66; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 256 GTTAACCTCCCTGCGAGCAAGTTAAGAGTGTGGGTACGACGGGATAGTGAACCGCAAT 315
Db 906 GATTAACCTACTATCTGCTCTTCAGAGAGACGTAACGTTGTGCATATACGATTCCTCAAT 965

Qy 316 GGTGCGTTTGGGTATCAACATCACCATAAGAAATGACGATCCACTCCCTAT 368
Db 966 AATGCGATTTGGGCAACCGGCAACCAACGTTTGGAAATGCTGAATCACTGTTAT 1018

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Qy 463 GGACTATTCCGACCGACCTCAACCTGGTGTGTCATGACGACAAATCTCGTATTGAT 522
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 Db 3851 GGTACACATCAACTACAACTCATCGTGTCTGCGAGAGTGAAGATCTAGGAACCAA 3792
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 Qy 523 ATGCCGATTTATGACATATGTCACGTGGGAGAGTACTCACTCTGTCGCTTCATG 582
 |||||
 Db 3791 ATGTCCTTTGCTGCTAAACACTTGGTAAAGTCATTACCTTTCTAGCAACAAGTTGCAATTTG 3732
 |||||
 Qy 583 GGTTCCTTCGGTTCAGATGAACGA 607
 |||||
 Db 3731 GGTTCCTTCAGTATCATATGAACCAA 3707
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RESULT 15

AC155611 AC155611 181924 bp DNA linear HTG 25-JAN-2005
 LOCUS Zea mays strain B73 clone ZMBB0283N16, *** SEQUENCING IN PROGRESS
 DEFINITION *** 10 unordered pieces.

ACCESSION AC155611

VERSION AC155611.2 GI:58082470

KEYWORDS HTG; HTGS_PHASE1.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 181924)

Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
 Uterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
 Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
 Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
 Quackenbush, J.

Consortium for Maize Genomics - BAC skim sequencing and assembly
 Unpublished

2 (bases 1 to 181924)

Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
 Uterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
 Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
 Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
 Quackenbush, J.

Direct Submission

Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),
 9712 Medical Center Dr, Rockville, MD 20850

3 (bases 1 to 181924)

Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
 Uterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
 Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
 Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
 Quackenbush, J.

Direct Submission

Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR),
 9712 Medical Center Dr, Rockville, MD 20850

On Jan 25, 2005 this sequence version replaced gi:57863132.

Trace submission

Center name: TIGR

Seq_id: ZGBC

Project information

Web site: <http://www.tigr.org/tdb/cgi/maize/>

Contact: maize@tigr.org

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 10 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 2052: contig of 2052 bp in length

* 2053 2152: gap of unknown length

* 2153 16425: contig of 14273 bp in length

* 16426 16525: gap of unknown length

* 16526 46015: contig of 29490 bp in length
 * 46016 46115: gap of unknown length
 * 46116 56214: contig of 10099 bp in length
 * 56215 56314: gap of unknown length
 * 56315 64697: contig of 8383 bp in length
 * 64698 64797: gap of unknown length
 * 64798 106326: contig of 41528 bp in length
 * 106326 173004: gap of unknown length
 * 173005 173104: contig of 66579 bp in length
 * 173105 175753: contig of 2649 bp in length
 * 175754 175853: gap of unknown length
 * 175854 178786: contig of 2933 bp in length
 * 178787 178886: gap of unknown length
 * 178887 181924: contig of 3038 bp in length.

FEATURES

source

1. 181924
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 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMBB0283N16"
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 /estimated_length=unknown
 16426..16525
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 56215..56314
 /estimated_length=unknown
 64698..64797
 /estimated_length=unknown
 106326..106425
 /estimated_length=unknown
 173005..173104
 /estimated_length=unknown
 175754..175853
 /estimated_length=unknown
 178787..178886
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ORIGIN

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 Best Local Similarity 53.8%; Pred. No. 4.3;
 Matches 78; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
 Qy 463 GGACTATTCCGACCGACCTCAACCTGGTGTGTCATGACGACAAATCTCGTATTGAT 522
 |||||
 Db 129335 GGTACACATCAATCTCAACATCCATGCTCTGCGAGAGTGAAGATCTAGGAACCAA 129394
 |||||
 Qy 523 ATGCCGATTTATGACATATGGTCACGTGGGCGAGCATCTACCTTGTGCTTCATG 582
 |||||
 Db 129395 ATGTCCTTTGTGCTAAACACTTGGTAAAGTCATTACCTTCTAGCAACAAGTTGCAATTTG 129454
 |||||
 Qy 583 GGTTCCTTCGGTTCAGATGAACGA 607
 |||||
 Db 129455 GGTTCCTTCAGTATCATATGAACCAA 129479
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Search completed: April 12, 2006, 08:18:12

Job time : 3616 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 12, 2006, 06:54:15 ; Search time 491 Seconds
(without alignment)
8429.275 Million cell updates/sec

Title: US-10-784-592-18_COPY_124_744

Perfect score: 621

Sequence: 1 aacacgtgtatgatctgcg.....aaacgacgtatgctcttcgcg 621

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|---------------------|
| 1 | 621 | 100.0 | 621 | 14 AEB45582 | Aeb45582 Alicyclob |
| 2 | 621 | 100.0 | 744 | 14 AEB45544 | Aeb45544 Alicyclob |
| 3 | 621 | 100.0 | 744 | 14 AEB48730 | Aeb48730 Alicyclob |
| c 4 | 37.4 | 6.0 | 2000 | 8 ADA71938 | Ada71938 Rice gene |
| 5 | 36.2 | 5.8 | 2306 | 8 ACC47595 | Acc47595 Gastrodia |
| 6 | 35.6 | 5.7 | 7636 | 5 ABA17217 | Abal17217 Human ner |
| c 7 | 35.2 | 5.7 | 580 | 10 ADK56798 | Adk56798 Plant DNA |
| 8 | 35 | 5.6 | 2349 | 13 ADS61627 | Ads61627 Bacterial |
| 9 | 35 | 5.6 | 42488 | 4 AAK66772 | Aak66772 Human imm |
| 10 | 34 | 5.5 | 2000 | 11 ACL37108 | Ac137108 Rice stre |
| 11 | 33.8 | 5.4 | 729 | 13 ADX12170 | Adx12170 Plant ful |
| 12 | 33.8 | 5.4 | 860 | 13 ADX12259 | Adx12259 Plant ful |
| c 13 | 33.4 | 5.4 | 706 | 10 ADK56319 | Adk56319 Plant DNA |
| 14 | 33.2 | 5.3 | 2000 | 8 ADA71938 | Ada71938 Rice gene |
| c 15 | 33.2 | 5.3 | 7480 | 13 ADP25286 | Adp25286 PRO polyp |
| c 16 | 33.2 | 5.3 | 7480 | 14 ADY17856 | Ady17856 DNA encod |
| c 17 | 32.6 | 5.2 | 2700 | 5 AAD14385 | Aad14385 Mouse bon |
| c 18 | 32.4 | 5.2 | 813 | 8 ACA28717 | Aca28717 Prokaryot |
| c 19 | 32.4 | 5.2 | 18595 | 4 AAS33411 | Aas33411 DNA encod |

| | | | | | |
|------|------|-----|--------|----------------|--------------------|
| c 20 | 32.4 | 5.2 | 49999 | 2 AAZ23899 | Aaz23899 Human LOB |
| 21 | 32.4 | 5.2 | 301477 | 13 ABD33362 | Abd33362 Human can |
| c 22 | 32.2 | 5.2 | 123526 | 10 ADJ79962 | Adj79962 Human gli |
| 23 | 32 | 5.2 | 26147 | 4 ABL11324 | Ab11324 Drosophil |
| c 24 | 31.8 | 5.1 | 534 | 6 ABQ55323 | Abq55323 Human ova |
| c 25 | 31.8 | 5.1 | 83432 | 14 AEA61124_3 | Continuation (4 of |
| 26 | 31.8 | 5.1 | 110000 | 14 ADZ45062_07 | Continuation (8 of |
| c 27 | 31.6 | 5.1 | 704 | 10 ADK58633 | Adk58633 Plant DNA |
| c 28 | 31.6 | 5.1 | 1007 | 10 ADK56823 | Adk56823 Plant DNA |
| 29 | 31.6 | 5.1 | 2000 | 11 ACL35887 | Ac135887 Rice stre |
| 30 | 31.6 | 5.1 | 110000 | 10 ACF67367_48 | Continuation (49 o |
| 31 | 31.6 | 5.1 | 110000 | 10 ACF67367_49 | Continuation (50 o |
| 32 | 31.6 | 5.1 | 110000 | 10 ACF65387_0 | Acf65387 Photorhab |
| c 33 | 31.4 | 5.1 | 1412 | 13 ADR65009 | Adr65009 Cotton cd |
| 34 | 31.4 | 5.1 | 1572 | 3 AAZ53068 | Aaz53068 Neisseria |
| 35 | 31.4 | 5.1 | 1848 | 10 ABZ38315 | Abz38315 N. gonorr |
| 36 | 31.4 | 5.1 | 1851 | 3 AAZ53069 | Aaz53069 Neisseria |
| 37 | 31.4 | 5.1 | 3531 | 12 ADQ63920 | Adq63920 Novel hum |
| 38 | 31.4 | 5.1 | 9547 | 6 ABL33505 | Ab133505 Human imm |
| c 39 | 31.4 | 5.1 | 12077 | 3 AAA81734 | Aaa81734 N. mening |
| c 40 | 31.4 | 5.1 | 17000 | 6 AAL40299 | Aal40299 Caspase 6 |
| 41 | 31.4 | 5.1 | 110000 | 3 AAA81489_6 | Continuation (7 of |
| 42 | 31.4 | 5.1 | 349980 | 3 AAF21612 | Aaf21612 Neisseria |
| 43 | 31.2 | 5.0 | 1173 | 12 ADJ34811 | Adj34811 DNA encod |
| c 44 | 31.2 | 5.0 | 6070 | 6 ABL33678 | Ab133678 Human imm |
| c 45 | 31.2 | 5.0 | 6070 | 6 ABL34578 | Ab134578 Human met |

ALIGNMENTS

RESULT 1

AEBA45582
ID AEB45582 standard; DNA; 621 BP.

XX AEB45582;

XX AC

DT 22-SEP-2005 (first entry)

XX Alicyclobacillus sp. mature functional polypeptide DNA (bases 124-744).
XX Feedstuff; food; detergent; surfactant; pulp; functional polypeptide;
XX gene; ds.

XX Alicyclobacillus sp.; DSM 15716.

XX Key Location/Qualifiers

FT CDS 1..621
FT /*tag= a
FT /product= "Alicyclobacillus sp. mature functional
FT polypeptide"
FT /partial
FT /note= "No start and stop codons"

XX US2005147983-A1.

XX 07-JUL-2005.

XX 23-FEB-2004; 2004US-00784592.

XX 06-JAN-2004; 2004DK-00000010.

XX 04-FEB-2004; 2004DK-00000165.

XX (NOVO) NOVOZYMES AS.

XX Wilting R, Lassen SP, Ostergaard PR;

XX WPI; 2005-511773/52.

XX P-PSDB; AEB45583.

XX New functional polypeptides having function and amino acid sequence
XX similar to known specific bacterial enzymes useful in industrial,
XX research and household applications e.g. detergents and food.

XX Claim 1; Page 7-8 (Disclosure); 1lpp; Chinese.
PS The invention relates to a fungus-inducible promoter from the plant
CC *Gastrodia elata*. The promoter is that of the *Gastrodia* antifungal protein
CC (GAPP) gene which is expressed in the tubers of the plant. The fungus-
CC inducible promoter may be used in transgenic plants to mediate expression
CC of heterologous genes in the presence of fungus. The present sequence
CC represents the GAPP gene sequence which includes its promoter
XX
SQ Sequence 2306 BP; 735 A; 416 C; 441 G; 714 T; 0 U; 0 Other;

Query Match 5.8%; Score 36.2; DB 8; Length 2306;
Best Local Similarity 57.5%; Pred. No. 0.89;
Matches 65; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 256 GTTAACCTCCCTGACGAGTTAAGAGTGTGGGTACGACGGGATAGTGAACCGCAAT 315
Db 1631 GGTAACCTACTATCTGATCTTTCAGAGAGATCGTAACTGCTCATATACGATAATTCAT 1690

Qy 316 GGTGGTGTGGTTATCAACATCACCATAGAAATGACGGATCCACTCTTAT 368
Db 1691 AATCGATTTGGCAACCCACCAACCGTTGGAATGCTGAAATCACTGTCTAT 1743

RESULT 6
ABAI17217
ID ABAI17217 standard; DNA; 7636 BP.
AC ABAI17217;
XX
XX
DT 23-JAN-2002 (first entry)
XX
XX Human nervous system related polynucleotide SEQ ID NO 9548.
XX
XX Human; neurotropic; cytotstatic; dermatological; virucide;
XX immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
XX antiparkinsonian; antischlicking; antianaemic; antiarthritic; cancer;
XX antineumatic; hepatotropic; cerebroprotective; antiinflammatory;
XX antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
XX antiparasitic; cardiac; immune disorder; cardiovascular disorder;
XX neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
OS Homo sapiens.
XX
XX WO200159063-A2.
XX
XX 16-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001334.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 24-FEB-2000; 2000US-0184664P.
XX 02-MAR-2000; 2000US-0186350P.
XX 16-MAR-2000; 2000US-0189874P.
XX 17-MAR-2000; 2000US-0190076P.
XX 18-APR-2000; 2000US-0198123P.
XX 19-MAY-2000; 2000US-0205515P.
XX 07-JUN-2000; 2000US-0209457P.
XX 28-JUN-2000; 2000US-0214886P.
XX 30-JUN-2000; 2000US-0215135P.
XX 07-JUL-2000; 2000US-0216647P.
XX 07-JUL-2000; 2000US-0216880P.
XX 11-JUL-2000; 2000US-0217487P.
XX 11-JUL-2000; 2000US-0217496P.
XX 14-JUL-2000; 2000US-0218290P.
XX 26-JUL-2000; 2000US-0220963P.
XX 26-JUL-2000; 2000US-0220964P.
XX 14-AUG-2000; 2000US-0224518P.
XX 14-AUG-2000; 2000US-0224519P.
XX 14-AUG-2000; 2000US-0225213P.
XX 14-AUG-2000; 2000US-0225214P.
XX 14-AUG-2000; 2000US-0225216P.
XX 14-AUG-2000; 2000US-0225267P.
XX 14-AUG-2000; 2000US-0225270P.
XX 14-AUG-2000; 2000US-0225447P.
XX 14-AUG-2000; 2000US-0225757P.
XX 14-AUG-2000; 2000US-0225758P.
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XX 18-AUG-2000; 2000US-0226279P.
XX 22-AUG-2000; 2000US-0226681P.
XX 22-AUG-2000; 2000US-0226868P.
XX 22-AUG-2000; 2000US-0227182P.
XX 23-AUG-2000; 2000US-0227009P.
XX 30-AUG-2000; 2000US-0228924P.
XX 01-SEP-2000; 2000US-0229287P.
XX 01-SEP-2000; 2000US-0229343P.
XX 01-SEP-2000; 2000US-0229344P.
XX 01-SEP-2000; 2000US-0229345P.
XX 05-SEP-2000; 2000US-0229509P.
XX 05-SEP-2000; 2000US-0229513P.
XX 06-SEP-2000; 2000US-0230437P.
XX 06-SEP-2000; 2000US-0230438P.
XX 08-SEP-2000; 2000US-0231242P.
XX 08-SEP-2000; 2000US-0231243P.
XX 08-SEP-2000; 2000US-0231244P.
XX 08-SEP-2000; 2000US-0231413P.
XX 08-SEP-2000; 2000US-0231414P.
XX 08-SEP-2000; 2000US-0232080P.
XX 12-SEP-2000; 2000US-0231968P.
XX 14-SEP-2000; 2000US-0232397P.
XX 14-SEP-2000; 2000US-0232398P.
XX 14-SEP-2000; 2000US-0232399P.
XX 14-SEP-2000; 2000US-0232400P.
XX 14-SEP-2000; 2000US-0232401P.
XX 14-SEP-2000; 2000US-0233063P.
XX 14-SEP-2000; 2000US-0233064P.
XX 21-SEP-2000; 2000US-0233065P.
XX 21-SEP-2000; 2000US-0234223P.
XX 25-SEP-2000; 2000US-0234274P.
XX 25-SEP-2000; 2000US-0234997P.
XX 25-SEP-2000; 2000US-0234998P.
XX 26-SEP-2000; 2000US-0235484P.
XX 27-SEP-2000; 2000US-0235834P.
XX 27-SEP-2000; 2000US-0235836P.
XX 29-SEP-2000; 2000US-0236327P.
XX 29-SEP-2000; 2000US-0236367P.
XX 29-SEP-2000; 2000US-0236368P.
XX 29-SEP-2000; 2000US-0236369P.
XX 29-SEP-2000; 2000US-0236370P.
XX 02-OCT-2000; 2000US-0236802P.
XX 02-OCT-2000; 2000US-0237037P.
XX 02-OCT-2000; 2000US-0237038P.
XX 02-OCT-2000; 2000US-0237039P.
XX 02-OCT-2000; 2000US-0237040P.
XX 13-OCT-2000; 2000US-0239935P.
XX 13-OCT-2000; 2000US-0239937P.
XX 20-OCT-2000; 2000US-0240960P.
XX 20-OCT-2000; 2000US-0241785P.
XX 20-OCT-2000; 2000US-0241786P.
XX 20-OCT-2000; 2000US-0241787P.
XX 20-OCT-2000; 2000US-0241808P.
XX 20-OCT-2000; 2000US-0241809P.
XX 20-OCT-2000; 2000US-0241826P.
XX 01-NOV-2000; 2000US-0242221P.
XX 08-NOV-2000; 2000US-0244617P.
XX 08-NOV-2000; 2000US-0246474P.
XX 08-NOV-2000; 2000US-0246475P.
XX 08-NOV-2000; 2000US-0246476P.
XX 08-NOV-2000; 2000US-0246477P.
XX 08-NOV-2000; 2000US-0246478P.
XX 08-NOV-2000; 2000US-0246523P.
XX 08-NOV-2000; 2000US-0246524P.

CC DNA sequence of the invention.

XX Sequence 580 BP; 160 A; 102 C; 148 G; 170 T; 0 U; 0 Other;

SQ

Query Match 5.7%; Score 35.2; DB 10; Length 580;

Best Local Similarity 53.7%; Pred. No. 1;

Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 325 TGGGTATCAACATCACCATAAGAAATGACGGATCCACTCTATGAGAGTCTGTTGATGGC 384

Db 194 TGGGATGACTAGCTTCCCTTAACAGGCTGAAACCACTATTGTAGGCCCTTGAATTGC 135

Qy 385 ATATTCCATTGCGAGACTTAACCGGAACGTTTATCAGCGGATCTTACTGCTGAGATA 444

Db 134 TCTCTCTTTTCCCGAAGTACATATGACCTGCTCTCTGCAAGCTGCGAGAAGAGAGAA 75

Qy 445 TATGCAATAACAAATT 460

Db 74 TGAAGCAACACAAATT 59

RESULT 8

ID ADS61627 standard; cDNA; 2349 BP.

XX ADS61627;

XX 02-DEC-2004 (first entry)

XX Bacterial polynucleotide #13614.

XX Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

KW pathogen tolerance; pest tolerance; plant disease resistance;

KW cell cycle pathway modification; plant growth regulator;

KW homologous recombination; seed oil yield; protein yield; carbohydrate;

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

KW bacterial polynucleotide; gene; ss.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI, 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide

PT for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 37301; 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a

CC promoter functional in a plant cell, where the promoter is positioned to

CC provide for expression of a polynucleotide encoding a polypeptide from a

CC microbial source. The invention also relates to a transformed plant

CC comprising the recombinant DNA construct and a method of producing a

CC transformed plant having an improved property. The plant is a crop plant

CC such as maize or soybean. The method of producing a transformed plant

CC having an improved property comprises transforming a plant with the

CC recombinant DNA construct and growing the transformed plant, where the

CC polynucleotide or polypeptide is useful for improving plant properties.

CC The recombinant DNA construct is useful for producing plants with

CC improved plant properties, e.g. improved cold, heat or drought tolerance,

CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,

CC increased resistance to plant disease, better growth rate by modification

CC of the cell cycle pathway with plant growth regulators, increased rate of

CC homologous recombination, modified seed oil or protein yield and/or

CC content, improved yield by modification of carbohydrate, nitrogen or

CC phosphorus use and/or uptake, by modification of photosynthesis or by

CC providing improved plant growth and development under at least one stress

CC condition. This sequence represents a bacterial polynucleotide used in

CC production. The scope of the invention. Note: The sequence data for this patent did

CC not form part of the printed specification but was obtained in electronic

CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX

SQ Sequence 2349 BP; 799 A; 436 C; 546 G; 568 T; 0 U; 0 Other;

Query Match 5.6%; Score 35; DB 13; Length 2349;

Best Local Similarity 55.3%; Pred. No. 2.3;

Matches 68; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 292 GACGGATAGGTGAACCGCAAAATGGTGGCTTTTGGGTATCAACATCACCATAAGAAAT 351

Db 1330 GACGGACAAGTGGAAACACGGAGTGCCCAATACCGCTCACCATAATACAAAAAAGGC 1389

Qy 352 GACGGATCCACTCCTATGAGAGTGGTGGTATTCATTTGCGAGAACTTAAACGGG 411

Db 1390 AAGTATCTATGCTAATGGAGGATGAAGTGTACATACGACGAAATGCTCAAACTAAACGCA 1449

Qy 412 AAC 414

Db 1450 AAC 1452

RESULT 9

AAK66772

ID AAK66772 standard; DNA; 42488 BP.

XX AAK66772;

XX 06-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21584.

DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

XX cytostatic; gene therapy; vaccine; metastasis; ds.

XX Homo sapiens.

OS

XX WO200157182-A2.

PN

XX 09-AUG-2001.

PD

XX 17-JAN-2001; 2001WO-US001354.

PF

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209457P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PS Claim 1; SEQ ID NO 6745; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a

CC polynucleotide consisting of a sequence encoding an amino acid sequence

CC available in electronic form from the US patent office at

CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide

CC of the invention are also useful in physical arrays of molecules and as

CC plant breeding markers. The recombinant DNA construct is useful for

CC improving plant tolerance to cold, heat, drought, herbicides, extreme

CC osmotic conditions, pathogens or pests, for manipulating growth rate in

CC plant cells by modification of the cell cycle pathway, for conferring

CC increased resistance to plant disease, for producing galactomannan,

CC lignin or plant growth regulators, for increasing the rate of homologous

CC recombination in plants, for improving yield by modification of

CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

CC or by providing improved plant growth and development under at least one

CC stress condition or for modifying seed oil or protein yield and/or

CC content. This sequence represents a plant full length insert

CC polynucleotide that can be used in the recombinant DNA construct of the

CC invention.

XX

SQ Sequence 729 BP; 208 A; 152 C; 171 G; 198 T; 0 U; 0 Other;

Query Match 5.4%; Score 33.8; DB 13; Length 729;

Best Local Similarity 52.5%; Pred. No. 3.4;

Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 461 CAGGAGCTATTCCGACCGACCTCAACCCCTGGTGTGTCATGACGACAAATCTCGTATTG 520

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

464 CTGGGCATATCTGCACCGGAGTACAAAGCCGAGTGCCTCAACGATGTTAGGAATGGG 523

Qy 521 ATATGCCGGATTTTATGACATATGTCACGTCGGGCGAGCATTTACTCACTTGTGCTTCCA 580

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

524 TTTCACGGGATCCCTCTCTGATATTACGTCGTCGAGAGAAATTACGTAGTGCCTCCTA 583

Qy 581 TGGGTTTCTTCGGGTCAGATG 601

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

584 TGAGTGTAGGCGGACGTACG 604

RESULT 12

ADX12259

ID ADX12259 standard; cDNA; 860 BP.

XX

AC ADX12259;

XX

XX 21-APR-2005 (first entry)

XX

XX Plant full length insert polynucleotide seqid 6834.

XX

XX plant protectant; plant growth regulant; gene therapy; plant;

XX recombinant DNA construct; physical array; plant breeding marker;

XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

XX extreme osmotic condition; pathogen tolerance; pest tolerance;

XX growth rate; cell cycle pathway; disease resistance;

XX galactomannan production; lignin production; plant growth regulator;

XX yield; plant growth; plant development; seed oil; protein yield;

XX protein content; gene; ss.

XX

XX Unidentified.

XX

XX US2004034888-A1.

XX

XX 19-FEB-2004.

XX

XX 28-APR-2003; 2003US-00425114.

XX

XX 06-MAY-1999; 99US-00304517.

XX

XX 05-NOV-2001; 2001US-00985678.

XX

XX (LIUJ/) LIU J.

XX (ZHOU/) ZHOU Y.

XX (KOVA/) KOVALIC D K.

XX

PA (SCRE/) SCREEN S E.

PA (TABAS/) TABASKA J E.

XX (CAOY/) CAO Y.

XX

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX

XX New recombinant DNA construct, useful for improving plant tolerance to

XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or

XX pests, for conferring increased resistance to plant disease, or for

XX improving yield.

XX

XX Claim 1; SEQ ID NO 6834; 15pp; English.

XX

XX The invention describes a recombinant DNA construct comprising a

XX polynucleotide consisting of a sequence encoding an amino acid sequence

XX available in electronic form from the US patent office at

XX ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide

XX of the invention are also useful in physical arrays of molecules and as

XX plant breeding markers. The recombinant DNA construct is useful for

XX improving plant tolerance to cold, heat, drought, herbicides, extreme

XX osmotic conditions, pathogens or pests, for manipulating growth rate in

XX plant cells by modification of the cell cycle pathway, for conferring

XX increased resistance to plant disease, for producing galactomannan,

XX lignin or plant growth regulators, for increasing the rate of homologous

XX recombination in plants, for improving yield by modification of

XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

XX or by providing improved plant growth and development under at least one

XX stress condition or for modifying seed oil or protein yield and/or

XX content. This sequence represents a plant full length insert

XX polynucleotide that can be used in the recombinant DNA construct of the

XX invention.

XX

SQ Sequence 860 BP; 220 A; 204 C; 245 G; 191 T; 0 U; 0 Other;

Query Match 5.4%; Score 33.8; DB 13; Length 860;

Best Local Similarity 52.5%; Pred. No. 3.6;

Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 461 CAGGAGCTATTCCGACCGACCTCAACCCCTGGTGTGTCATGACGACAAATCTCGTATTG 520

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

600 CTGGGCATATCTGCACCGGAGTACAAAGCCGAGTGCCTCAACGATGTTAGGAATGGG 659

Qy 521 ATATGCCGGATTTTATGACATATGTCACGTCGGGCGAGCATTTACTCACTTGTGCTTCCA 580

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

660 TTTCACGGGATCCCTCTCTGATATTACGTCGTCGAGAGAAATTACGTAGTGCCTCCTA 719

Qy 581 TGGGTTTCTTCGGGTCAGATG 601

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

720 TGAGTGTAGGCGGACGTACG 740

RESULT 13

ADK56319/c

ID ADK56319 standard; DNA; 706 BP.

XX

XX ADK56319;

XX

XX 06-MAY-2004 (first entry)

XX

XX Plant DNA sequence which confers altered metabolic characteristic #3702.

XX

XX altered metabolic characteristic; plant; acid metabolism;

XX alcohol metabolism; fatty acid metabolism;

XX branched fatty acid metabolism; alkaloid metabolism;

XX amino acid metabolism; ester metabolism; glyceride metabolism;

XX phenolic metabolism; carbohydrate metabolism; sterol metabolism;

XX terpene metabolism; isoprenoid metabolism; alkene metabolism;

XX alkyne metabolism; hydrocarbon metabolism; ketone metabolism;

XX quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.

XX

XX Unidentified.

| | |
|----|---|
| XX | WO20030209336-A1. |
| PN | |
| XX | 13-MAR-2003. |
| XX | |
| XX | 30-AUG-2002; 2002WO-US027884. |
| XX | |
| XX | 31-AUG-2001; 2001US-0316471P. |
| XX | |
| XX | (DOWC) DOW CHEM CO. |
| PA | (DOWC) DOW AGROSCIENCES LLC. |
| XX | |
| XX | Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ; |
| PI | Oriedo JVB, Croasley R, Reddy AS, Shukla V, Larrinua I, Miller BA; |
| PI | |
| XX | WPI; 2003-313091/30. |
| DR | |
| XX | Novel genes that confer altered metabolic characteristics in Nicotiana |
| XX | benthianaiana plants, useful for altering the levels of metabolites e.g. |
| PT | acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols. |
| PT | |
| XX | |
| XX | Claim 1; SEQ ID NO 3702; 2576pp; English. |
| PS | |
| XX | |
| CC | The invention comprises DNA sequences which confer an altered metabolic |
| CC | characteristic when they are expressed in a plant. The DNA sequences of |
| CC | the invention are useful for producing plants with an altered metabolic |
| CC | characteristic, such as: altered acid metabolism, alcohol metabolism, |
| CC | fatty acid metabolism, branched fatty acid metabolism, alkaloid or other |
| CC | base metabolism, altered amino acid metabolism, altered ester metabolism, |
| CC | altered glyceride metabolism, altered phenolic metabolism, altered |
| CC | carbohydrate metabolism, altered sterol, oxygenated terpene, or |
| CC | isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon |
| CC | metabolism, ketone or quinone metabolism. The DNA sequences of the |
| CC | invention may be used to provide disease resistance in a plant and gene |
| CC | shuffling or sexual PCR procedures. The present nucleic acid represents a |
| CC | DNA sequence of the invention. |
| XX | |
| XX | Sequence 706 BP; 180 A; 163 C; 143 G; 220 T; 0 U; 0 Other; |
| SQ | |

| Query Match | 5.4%; | Score 33.4; | DB 10; | Length 706; |
|-----------------------|-----------------|--|-----------|-------------|
| Best Local Similarity | 47.4%; | Pred. No. 4.5; | | |
| Matches 100; | Conservative 0; | Mismatches 111; | Indels 0; | Gaps 0; |
| Qy | 233 | AGGTAGGAGACTCGAAATTAGAGTTAACTCCCTGCAGCAGTTAAAGAGTGTGGGGTACG | 292 | |
| Db | 578 | ATGCAGGACGTTGATGATTTTTTGTCATCCACCATCTTCATTGTAAGGTGTATGATCCCA | 519 | |
| Qy | 293 | ACGGGATAGGTGAAACCGCAAAATGGTGGTTTTGGGTATCAACATCACCATTAAGAAATG | 352 | |
| Db | 518 | GGTGGAGTAAATCCAGGCAACTCTTGTGAGTGGGAAATCAAAAATCACCGAAGCTGGG | 459 | |
| Qy | 353 | ACGGATCCACTCCTATGAGGTCGTGATGGCATATTCCAATTCAGAGAACTTTAAACGGGA | 412 | |
| Db | 458 | CACGATGTCTCTTTACATAGGTGCATGGCCCTCGTGGTGCATCGAAGAACAAATAGTTTA | 399 | |
| Qy | 413 | ACGTTTATCAGCCGGATTCTACTCTGAGAT | 443 | |
| Db | 398 | ACATCAATCACAGCTTTCTCCGGTGAGAT | 368 | |

RESULT 14

ADA71938
ID ADA71938 standard; DNA: 2000 BP.

ADA71938:

20-NOV-2003 (first entry)

DE Rice gene. SEO ID 5263.

Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene: ds.

XXV

| | |
|----|--------------------|
| OS | Oryza sativa. |
| XX | WO2003000898-A1. |
| PN | 03-JAN-2003. |
| XX | 22-JUN-2001; 2003 |
| PD | 22-JUN-2001; 2003 |
| XX | (SYGN) SYNGENTAF |
| PF | Chang H, Chen W |
| XX | Katagiri F, Qu |
| XX | WPI; 2003-175290 |
| PA | Identifying at l |
| PI | pathogenic infec |
| PI | bacterial, funga |
| XX | gene expression. |
| DR | Claim 27; SEQ ID |
| XX | The present inven |
| XX | involved in plan |
| CC | comprises ident |
| CC | the incompatibil |
| CC | expression of th |
| CC | does not corres |
| CC | or in a correspond |
| CC | useful for conf |
| CC | bacterial, funga |
| CC | illustrate the i |
| XX | Sequence 2000 BP |

| | | | | |
|-----------------------|-------------------|-----------------|-----------|--------------|
| Query Match | 5.3% | Score 33.2; | DB 8; | Length 2000; |
| Best Local Similarity | 7.7% | Pred. NO. 8.3; | | |
| Matches 38; | Conservative 234; | Mismatches 212; | Indels 8; | Gaps 1; |

| | | | |
|----|-----|--|-----|
| Qy | 6 | GGTGTATATGATTCGAGGAAACACACCGCGGAACGCATCAACGCTAAGCGCTCAACTTC | 65 |
| Db | 96 | RSKRRGRGRGRMRSRMRWGRYRRCARSGRWAGSGRMGGKSRMSYMMWCYARGCS | 155 |
| Qy | 66 | TTTGGTTAAATTCGACAGAAATAGTTTCACAGGTAGCAAGACAAGAGACAAATTCGAGTACGTC | 125 |
| Db | 156 | CKRKSKGSGWKTCCRARGGSGWSSGAKYKSGSMSKRWMMSSCGRSGCRRSAYSRY | 215 |
| Qy | 126 | TCCCGCTCATAAAGTCTTAGCAACTCATTTGCAACATGCGCAACATCAAGCTGCTACGACTTC | 185 |
| Db | 216 | GTSRKYGTYYKQMTYVSASRCWRAVMTTYSYSAWCSSYTWCRSKRSMWMMKMRKMRSSRY | 275 |
| Qy | 186 | ATCTTCTCAGTCGAAGTTACGATATATCCCGT-----TTCAACATACAGGGAAGGTA | 237 |
| Db | 276 | GWTSWSTYMMWMTAYKKSYYSRNCYMTTGGGWRGATRYWGRGYSRNMWMTKQMTYRGY | 335 |
| Qy | 238 | GGAGACTTGGAAATATAGAGTTAACTCCCTCGACGAAGTTAAGAGTGTGGGGTACGACGG | 297 |
| Db | 336 | KGMKRGWAGRMWRSMCRWSKACYMRWRMRWTRRRRWRWAKGSSRTSRKKRKCWKMR | 395 |
| Qy | 298 | ATAGGTGAACCGCAATGGTGGCTTTTGGGTATCAACATCAACATCAAGAAATGACGGA | 357 |
| Db | 396 | KYKMRGYSRMRSCKRMMKRCRSGRAWKMGRCGCMTCRMKSYGMMRWKSWKRMASKYK | 455 |
| Qy | 358 | TCCACTCTATGAGAGTTCGTTGATGGCATATTCATTTGCAAGCACTTTAAACCGGGAAGCTT | 417 |
| Db | 456 | WMSRMYRKKCKSPRTTWGKTRGMMGTWGRCTFYKBSGMKRCRRRWRGWRMYRMEWR | 515 |
| Qy | 418 | TATCAGCCGGATTCCTACTGCTGGAGATATATGCAAAATACAAATTCCAGGACTATTTCCGACC | 477 |
| Db | 516 | YMSRYTMYRCARKKQTSYAARKCARCWYRGKGYWAGMMWKRYKMYMTKOMMMYKRYK | 575 |

Oryza sativa.
WO2003000898-A1.
03-JAN-2003.
22-JUN-2001; 2001WO-IB001105.
22-JUN-2001; 2001WO-IB001105.
(SYGN) SYNGENTA PARTICIPATIONS AG

Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y, Katagiri F, Qian S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G; WPI: 2003-175290/17.

Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.

Claim 27: SGO ID NO 5263: 899pp: English:

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

Query Match 5.3%; Score 33.2; DB 8; Length 2000;
Best Local Similarity 7.7%; Pred. No. 8.3;
Matches 38; Conservative 234; Mismatches 212; Indels 8

| | | | |
|----|-----|--|-----|
| Qy | 6 | GGTGTATATGATTCGAGGAAACACACCGCGGAACGCATCAACGCTAAGCGCTCAACTTC | 65 |
| Db | 96 | RSKRRGRGRGRMRSRMRWGRYRRCARSGRWAGSGRMGGKSRMSYMMWCYARGCS | 155 |
| Qy | 66 | TTTGGTTAAATTCGACAGAAATAGTTTCACAGGTAGCAAGACAAGAGACAAATTCGAGTACGTC | 125 |
| Db | 156 | CKRKSKGSGWKTCCRARGGSGWSSGAKYKSGSMSKRWMMSSCGRSGCRRSAYSRY | 215 |
| Qy | 126 | TCCCGCTCATAAAGTCTTAGCAACTCATTTGCAACATGCGCAACATCAAGCTGCTACGACTTC | 185 |
| Db | 216 | GTSRKYGTYYKQMTYVSASRCWRATMTTYSWACSSYTWCRSKRSMWMMWRKMRWSRSY | 275 |
| Qy | 186 | ATCTTCTCAGTCGAAGTTACGATATATCCCGT-----TTCAACATACAGGGAAGGTA | 237 |
| Db | 276 | GWTSWSTYMMWMTAYKKSYTSRMCYTRGGGRGATRYWGRGYMSRWMMTKQMTYRGY | 335 |
| Qy | 238 | GGAGACTTGGAAATTAGAGTTAACTCCCTCGACGAAGTTAAGAGTGTGGGGTACGACGG | 297 |
| Db | 336 | KGMRGWGWRMMRSMCRWSKACYMRWRMRWTRRRRWRWAKGSSRTSRKKRKCWKMR | 395 |
| Qy | 298 | ATAGGTGAACCGCAATGGTGGCTTTTGGGTATCAACATCAACATCAAGAAATGACGGA | 357 |
| Db | 396 | KYKMRGYSMRSCIKRWMKRCRSGRAWKMGCRGCMTCRMKSYGMMRWKSWKRMASKYK | 455 |
| Qy | 358 | TCCACTCTAGAGGTGCTTGTATGGCATATTCATTTGCAAGACTTTAAACGGGAAGCTT | 417 |
| Db | 456 | WMSBYMRKKCKSPRTTWGKTRGMMGTWGRCTFYKBSGMKRCRRRWGRBMYRMEWR | 515 |
| Qy | 418 | TATCAGCGCGGATTTACTGCTGGAGATATATGCAAAATACAAATTCAGGAGCACTATTCGAC | 477 |
| Db | 516 | YMSAYTMRYCARKKYSYAARKCARCWYRGKGYWAGMMWKRYKMYMTKOMMMYKRYK | 575 |

QY 478 GACCTCAACCCCT 489
: | :: ::
Db 576 SKCSWYCKMSYY 587

RESULT 15

ADP25286/c
ID ADP25286 standard: cDNA: 7480 BP.

AC ADP25286:

18-NOV-2004 (first entry)

DE PRO polypeptide encoding cdNA SEQ ID NO:2464.

ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
 KW immunosuppressive; osteopathic; antidiabetic; dermatological;
 KW antipsoriatic; antiallergic; antisthmatic; hepatotropic; respiratory;
 KW gene therapy; immune system.

Unidentified.

XX PN WO2004041170-A2

21-MAY-2004

XX
PP 30-OCT-2003; 2003WO-US034312.

01-NOV-2002; 2002US-0423394P.

PA (GETH) GENENTECH INC.

PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;

WPI: 2004-419628/39.

New PRO polypeptides and polynucleotides, useful for treating e.g. PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated PT renal disease, or demyelinating diseases of the central or peripheral PT nervous system.

PG claim 1: SEQ ID NO 2464: 2940pp: English:

The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has anti-inflammatory, antiarthritis, antirheumatic, immunosuppressive, osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic, antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence encodes a PRO protein of the invention.

Sequence 7480 BP; 2277 A; 1271 C; 1472 G; 2460 T; 0 U; 0 Other;

| Query Match | 5.3% | Score 33.2; | DB 13; | Length 7480; |
|-----------------------|-----------------|--|-----------|--------------|
| Best Local Similarity | 44.8%; | Pred. No. 15; | | |
| Matches 128; | Conservative 0; | Mismatches 158; | Indels 0; | Gaps 0; |
| Qy | 18 | TCGAGGAAACACACCGGGNACGCATCAACGGTAAAGGCTACAACCTCTTTGGTTAAATTC | 77 | |
| Db | 2442 | TAGATGGAAGAAACTGCGAAAGACGCCCATTTTACTCCAAATCCATATCTTAAAGTAATTC | 2383 | |
| Qy | 78 | GACGAATAGTTCACAGGTAGCAAGCAAGCAAAAACCTCGAGTAGCGTCTCCCGCTCATAA | 137 | |
| Db | 2382 | TTTAGAAAAATTAGAAATAAAAAAGTAATAACACAAAAGATCTATTCCAAACATGCTT | 2323 | |
| Qy | 138 | GTCTACGAACCTCATTTGCAACATCGGCAACATCAAGCTGCTACGACTTCATCTTCTCAGTC | 197 | |
| Db | 2322 | GCCTTCTATACAATTATGTAGTATTAACTCTATTATATTACGGCTTATGATCGAGATTT | 2263 | |
| Qy | 198 | GAAGTTTACGATATATCCCGTTTCACACATACGGGAAGGTAGGAGACTTGGAATATTAGAGT | 257 | |
| Db | 2262 | GAATATCCTAAATAACATTTCCCAACAAATCAGGTATGGAGCATAAAGATATCATAAAGT | 2203 | |
| Qy | 258 | TAACCTCCTCGACGAAGTTAAGAGTGTGGGGTACGACGGGATAGGT | 303 | |
| Db | 2202 | ATRAACCTCTCAGCAGGTGCGAGTCTGTTGTGTCACACAGCAGCAGT | 2157 | |

Search completed: April 12, 2006. 08:35:25

Job time : 494 secs

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GENCORE VERSION 3.1.1

| Result No. | Query # | | | DB | ID | Description |
|------------|---------|-------|--------|----|----------|--------------------|
| | Score | Match | Length | | | |
| 1 | 39.8 | 6.4 | 444 | 1 | AU269824 | AU269824 AU269824 |
| 2 | 39.6 | 6.4 | 714 | 6 | CA996800 | CA996800 r903d03.y |
| 3 | 39.2 | 6.3 | 475 | 3 | BJ445212 | BJ445212 BJ445212 |
| 4 | 39.2 | 6.3 | 729 | 5 | BU364247 | BU364247 603785266 |
| 5 | 39.2 | 6.3 | 782 | 3 | BJ436673 | BJ436673 BJ436673 |
| 6 | 39 | 6.3 | 393 | 3 | BJ439058 | BJ439058 BJ439058 |
| 7 | 39 | 6.3 | 742 | 8 | DR070632 | DR070622 RTDKL 14 |
| 8 | 39 | 6.3 | 782 | 7 | CO167205 | CO167205 PLD1_67.C |
| 9 | 38.6 | 6.2 | 371 | 3 | BJ440426 | BJ440426 BJ440426 |
| 10 | 38.6 | 6.2 | 374 | 3 | BJ440571 | BJ440571 BJ440571 |
| 11 | 38.6 | 6.2 | 391 | 3 | BJ440677 | BJ440677 BJ440677 |
| 12 | 38.6 | 6.2 | 393 | 3 | BJ440820 | BJ440820 BJ440820 |
| 13 | 38.6 | 6.2 | 394 | 3 | BJ440720 | BJ440720 BJ440720 |
| 14 | 38.6 | 6.2 | 422 | 3 | BJ437922 | BJ437922 BJ437922 |
| 15 | 38.6 | 6.2 | 458 | 3 | BJ444032 | BJ444032 BJ444032 |
| 16 | 38.6 | 6.2 | 463 | 3 | BJ438307 | BJ438307 BJ438307 |
| 17 | 38.6 | 6.2 | 463 | 3 | BJ445358 | BJ445358 BJ445358 |
| 18 | 38.6 | 6.2 | 470 | 3 | BJ438852 | BJ438852 BJ438852 |
| 19 | 38.6 | 6.2 | 472 | 3 | BJ437919 | BJ437919 BJ437919 |
| 20 | 38.6 | 6.2 | 503 | 3 | BJ444250 | BJ444250 BJ444250 |
| 21 | 38.6 | 6.2 | 506 | 3 | BJ442298 | BJ442298 BJ442298 |
| 22 | 38.6 | 6.2 | 524 | 3 | BJ443637 | BJ443637 BJ443637 |

```

Qy 359 CCACTCTCTAGGAGTGTGGTATGATGGCATATTCCATTTGCGAACTTAAACGGGAACGTTT 418
Db 130 CTTTGTGTAATGATCNCAGGTTGGTTAGCTTACATTAATAAGGTTATGTTAAAGATG 189
Qy 419 ATCAGCGCGATTCTACTGCTGAGATATATGCAATACAAATTCAGGCACTATT 471
Db 190 CAACTTCAATGTTTACTGTTGGTGAAGTTTATGCTCATTCAATGCTGCTAAAAAT 242

RESULT 2
CA996800/c
LOCUS
DEFINITION
  iq30d03.y1 Meloidogyne hapla J2 pamp1 v1 Meloidogyne hapla cDNA 5'
  similar to TR:001685 001685 SIMILAR TO ALANINE AMINOTRANSFERASE.
  [] ; mRNA sequence.
ACCESSION
  CA996800
VERSION
  CA996800.1 GI:27541671
KEYWORDS
  EST.
SOURCE
  Meloidogyne hapla
  Meloidogyne hapla
  Meloidogyne hapla
REFERENCE
  1 Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.
  (bases 1 to 714)
AUTHORS
  McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
  Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
  Bowers,Y., Gibbons,M., Ritter,B., Bennett,J., Franklin,C.,
  Tsagarishvili,R., Konko,I., Kennedy,S., Maguire,L., Beck,C.,
  Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,Y.,
  Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
  McCann,R., Waterston,R. and Wilson,R.
  The Washington Univ. Nematode EST Project, 1999
  Unpublished (1999)
  Contact: McCarter JP
  The Washington Univ. Nematode EST Project, 1999
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  The library was constructed by Claire Murphy and Dr. James McCarter
  at Washington University, St. Louis. J2 were provided by Dr.
  Valerie Williamson of the University of California at Davis
  (vmwilliamson@ucdavis.edu).
  Seq primer: -40RP from Gibco
  High quality sequence stop: 414.
FEATURES
  source
  1. 714
  /organism="Meloidogyne hapla"
  /mol_type="mRNA"
  /db_xref="taxon:6305"
  /dev_stage="J2"
  /lab_host="DH10B"
  /clone_lib="Meloidogyne hapla J2 pamp1 v1"
  /note="Vector: pamp1 (Gibco) ; Site 1: NotI; Site 2: SalI;
  The library was constructed by Claire Murphy and Dr. James
  McCarter at Washington University, St. Louis. The cDNA was
  made by using Dynabead oligo-dr priming (Dynal). PCR based
  library using a modified protocol from the SMART PCR cDNA
  Synthesis Kit from Clontech. Directionally cloned into the
  UDG sites of pamp1. J2 were provided by Dr. Valerie
  Williamson of the University of California at Davis
  (vmwilliamson@ucdavis.edu)."
ORIGIN
  Query Match 6.4%; Score 39.6; DB 6; Length 714;
  Best Local Similarity 50.5%; Pred. No. 0.46;
  Matches 96; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 320 CGTTTGGTTATCAACATCAACATAAGAAATGACGATCCACTCTATGAGGTGTTG 379
Db 268 CATTGGATTAAATCGTCTCAACAGTAGACACACGCTTTCTCGCCAAATTTGAACGTG 209
Qy 380 ATGGCATATTCATTTGCGAACTTAAACGGGAACGTTTATCAGCCGGAATTTACTGCTG 439

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Db 208 TTGCATATTTCTGTTTATTTCACAATTAATAATGGTAAAGTCTTGTGTTGCGCTG 149
Qy 440 AGATATATGAATAATACAAATTCAGGCACTATTCCGACCGCACTCAACCCCTGGTGTCCA 499
Db 148 GAATATAAGTAAAAAACAGACAGTCGATATAATGCTGTCATCTCAAAGCTGTTGAATGCA 89
Qy 500 TGACGACAAA 509
Db 88 TTCAAAAAAA 79

RESULT 3
BJ445212/c
LOCUS
DEFINITION
  BJ445212 Dictyostelium discoideum cDNA library, VF Dictyostelium
  discoideum cDNA clone ddv5821 3', mRNA sequence.
ACCESSION
  BJ445212
VERSION
  BJ445212.1 GI:19419933
KEYWORDS
  EST.
SOURCE
  Dictyostelium discoideum
  Dictyostelium discoideum
  Dictyostelium discoideum
  Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE
  1 (bases 1 to 475)
AUTHORS
  Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
  Full length cDNA of Dictyostelium discoideum at the vegetative
  stage
  Unpublished (2002)
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp.
FEATURES
  source
  1. 475
  /organism="Dictyostelium discoideum"
  /mol_type="mRNA"
  /strain="AX4"
  /db_xref="taxon:44699"
  /clone="ddv5821"
  /sex="mat A"
  /dev_stage="Growth phase"
  /clone_lib="Dictyostelium discoideum cDNA library, VF"
ORIGIN
  Query Match 6.3%; Score 39.2; DB 3; Length 475;
  Best Local Similarity 51.4%; Pred. No. 0.55;
  Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 299 TAGGTGAACCGGCAATGCGTGGTTTGGTTCATCATCATCACCATAAGAATGACGGAT 358
Db 269 TGGTTGAAAAAGAAAAATAAAGTTAATGATATCAACAAACCGTATTANATGCGAAT 210
Qy 359 CCACCTCTATGAGGAGTGTGATGCGCATATTCCCATTTGCGAACTTAAACGGGAACGTTT 418
Db 209 CTTTGTGTAATGATCACCCAGGTGTTTAGCTTACATTAATAATGGTATTGTTAAAGATG 150
Qy 419 ATCAGCGCGAATTCATCTGCTGAGATATATGCAATACAAATTCAGGCACTATT 471
Db 149 CAACTTCAATGTTTACTGTTGGTGAAGTTTATGCTCATTCAATGCTGCTAAAAAT 97

RESULT 4
BU364247/c
LOCUS
DEFINITION
  BU364247 CSEQHN72 Gallus gallus cDNA clone CHEST740x15 5', mRNA
  sequence.
ACCESSION
  BU364247
VERSION
  BU364247.1 GI:25872248
KEYWORDS
  EST.
SOURCE
  Gallus gallus (chicken)

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ORGANISM      Gallus gallus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
TITLE          Phasianidae; Gallus.
JOURNAL        1 (bases 1 to 729)
PUBMED         Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
COMMENT        Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
                A Comprehensive Collection of Chicken cDNAs
                Curr. Biol. 12 (22), 1965-1969 (2002)
                12445392
                Contact: Simon Hubbard
                Department of Biomolecular Sciences
                University of Manchester Institute of Science and Technology
                (UMIST)
                PO Box 88, Manchester, M60 1QD, UK
                Tel: 0161208930
                Fax: 01612360409
                Email: Simon.Hubbard@umist.ac.uk.

FEATURES      source
               1..729
               /organism="Gallus gallus"
               /mol_type="mRNA"
               /strain="Compton Line 151"
               /db_xref="taxon:9031"
               /clone="ChEST740k15"
               /sex="Female"
               /tissue_type="cerebrum"
               /dev_stage="adult"
               /lab_host="DH10B"
               /clone_lib="CSEQCHN72"
               /note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
               EcoRI; Site_2: NotI; This normalized library was
               constructed from 1 million independent clones. cDNA
               synthesis was initiated using an oligo(dT) primer, using
               methylated C in the first strand synthesis reaction.
               Following this first strand reaction, double-stranded cDNA
               was blunted, ligated to NotI adapters, digested with
               EcoRI, size-selected, and cloned into the NotI and EcoRI
               compatible sites of a custom modified MCS of the
               pBluescript (KS+) vector. The library was normalized in 2
               rounds using conditions adapted from Soares et al., PNAS
               (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
               (1996): 791, except that a significantly longer
               reannealing hybridization was used."

ORIGIN
Query Match      6.3%; Score 39.2; DB 5; Length 729;
Best Local Similarity 52.4%; Pred. No. 0.63;
Matches 86; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 62 CTTCTTTGGTTAATTCGACGAATAGTTCACAGGTAGCAAGCAAGCAAACTCGAGTA 121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 387 CTTATTAGTGACTGTGTGCAATAGTTCACAAGATGTAGATGACAGCATAGTAAGGA 328

Qy 122 CGTCTCCCGCTCATAGTCTAGCAACTCATTCGAACATCGCGCAACATCAAGCTGTACGA 181
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 327 AGACACCCGACCTCGCCAGAAAGTGCCCTGCAACTCGTGAAGCTTCAGCAGCGCGGA 268

Qy 182 CTTGATCTCTCAGTCGAGGTACCATATATCCCGTTTCACACA 225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 AGTCAACCTGTGATAGTAACATTTTGTTCGCCCACTTCATTCA 224

RESULT 5
BJ436673/c
LOCUS
DEFINITION      BJ436673 Dictyostelium discoideum cDNA library, VF Dictyostelium
                discoideum cDNA clone ddv31120 3', mRNA sequence.
ACCESSION      BJ436673
VERSION        BJ436673.1
KEYWORDS       EST.
SOURCE         Dictyostelium discoideum
ORGANISM       Dictyostelium discoideum
```

```
ORGANISM      Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE      1 (bases 1 to 782)
AUTHORS        Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
TITLE          Full length cDNA of Dictyostelium discoideum at the vegetative
                stage
JOURNAL        Unpublished (2002)
COMMENT        Contact: Tadasu Shin-i
                Center For Genetic Resource Information
                National Institute of Genetics
                1111 Yata, Mishima, Shizuoka 411-8540, Japan
                Tel: 81-559-81-6856
                Fax: 81-559-81-6855
                Email: tshini@genes.nig.ac.jp.

FEATURES      source
               1..782
               /organism="Dictyostelium discoideum"
               /mol_type="mRNA"
               /strain="AX4"
               /db_xref="taxon:44689"
               /clone="ddv31120"
               /sex="mat A"
               /dev_stage="Growth phase"
               /clone_lib="Dictyostelium discoideum cDNA library, VF"

ORIGIN
Query Match      6.3%; Score 39.2; DB 3; Length 782;
Best Local Similarity 51.4%; Pred. No. 0.65;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 299 TAGGTGAACCGCAAAATGGTGCCTTTGGGTTATCATCATCACCATAGGAATGACCGAT 358
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 425 TGGTTGAAAAGAAAATAAAAAGTTAATGATATCAACAAACCGTATTAGATGCGAAT 366

Qy 359 CCACCTCTATGGAGGTGCTTGATGCGCATATTCCTATTTCAGCAACTTAAACCGGAACGTTT 418
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 365 CTTTGTGTTATGATCACCAGGTGGTTAGCTTACATTAAATGGGTATNGTTAAGATG 306

Qy 419 ATCAGCCGGATTCTACTGCTGAGATATATGCAAAATACAAATTCAGGGACTATT 471
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 305 CAACCTCAATGTTTACTTGGTGAAGTTTATGCTCATTCAATGCTGCTAAAAAT 253

RESULT 6
BJ439058/c
LOCUS
DEFINITION      BJ439058 Dictyostelium discoideum cDNA library, VF Dictyostelium
                discoideum cDNA clone ddv39f08 3', mRNA sequence.
ACCESSION      BJ439058
VERSION        BJ439058.1
KEYWORDS       EST.
SOURCE         Dictyostelium discoideum
ORGANISM       Dictyostelium discoideum
                Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE      1 (bases 1 to 393)
AUTHORS        Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
TITLE          Full length cDNA of Dictyostelium discoideum at the vegetative
                stage
JOURNAL        Unpublished (2002)
COMMENT        Contact: Tadasu Shin-i
                Center For Genetic Resource Information
                National Institute of Genetics
                1111 Yata, Mishima, Shizuoka 411-8540, Japan
                Tel: 81-559-81-6856
                Fax: 81-559-81-6855
                Email: tshini@genes.nig.ac.jp.

FEATURES      source
               1..393
               /organism="Dictyostelium discoideum"
               /mol_type="mRNA"
               /strain="AX4"
               /db_xref="taxon:44689"
               /clone="ddv39f08"
               /sex="mat A"
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/dev stage="Growth phase"
/clone_lib="Dictyostellium discoideum cDNA library, VF"

Query Match      6.3%; Score 39; DB 3; Length 393;
Best Local Similarity 50.0%; Pred. No. 0.6;
Matches 84; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 299 TAGGTGAACCGCAATGGTGGCTTTGGGTATCAACATCCATCAAGTAAGTACGGAT 358
Db 255 TGGTTGAAAAGNAAATAAAAGTTAATGATNATCAACAAACCGTATTAGATGNGAAT 196
Qy 359 CCACCTCTATGGAGTGGTGGTATGATGCATATTCATTTGCAGAACTTAAACCGGGAACGTTT 418
Db 195 CTTTGTATGATCNCACCGTGGTGTAGCTTACNNTAAATGGTATGTTGTTAAAGATG 136
Qy 419 ATCAGCGGATCTTACTGCTGAGATATATGCAATATCAAAATTCAGGGA 466
Db 135 CAATTCNATGTTTACTGGTGAAGTTTATGCTCATTCAAGNGCTGNTA 88

RESULT 7
DR070622
LOCUS      RTDK1_14_C03_g1_A029 Roots, dark Pinus taeda cDNA clone
DEFINITION RTDK1_14_C03_g1_A029 5', mRNA sequence.
ACCESSION  DR070622.1 GI:67048356
VERSION     RTDK1_14_C03_g1_A029 5', mRNA sequence.
KEYWORDS    EST.
SOURCE      Pinus taeda (loblolly pine)
ORGANISM    Pinus taeda
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE   1 (bases 1 to 742)
AUTHORS     Pratt,L., Cordonnier-Pratt,M.M., Lorenz,W.W., Zimmermann,C. and
            Dean,J.F.D.
TITLE       An EST database from dark-treated loblolly pine (Pinus taeda) roots
JOURNAL     Unpublished (2005)
COMMENT     Other_ESTs: RTDK1_14_C03.bl_A029
            Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            RNA prepared and library constructed by W. Walter Lorenz (School of
            Forest Resources, University of Georgia); plant material prepared
            by Craig Zimmermann (School of Forest Resources, University of
            Georgia) using rooted cuttings provided by the Forest Biology
            Research Cooperative (FBRC) and the CCLONES project a the
            University of Florida; sequencing done in the Laboratory for
            Genomics and Bioinformatics, University of Georgia. Sequence ends
            have been trimmed to exclude vector and regions below phred quality
            16. Three-prime sequences are presented as their reverse complement
            and have been trimmed to exclude polyA.
            Seq primer: JENREV (CAGAAACAGCTATGACC).
            Location/Qualifiers
                1..742
                /organism="Pinus taeda"
                /mol_type="mRNA"
                /strain="3 CCLONES"
                /db_xref="taxon:3352"
                /clone="RTDK1_14_C03_A029"
                /lab_host="DH10B-T1 phage-resistant E. coli"
                /clone_lib="Roots, dark"
                /note="Organ: Root; Vector: pSL1180; Site 1: ECORI;
                Site 2: XhoI; The library was prepared from polyA+ RNA
                from the roots of 1-year-old loblolly pine (Pinus taeda)
                cuttings that were rooted and then planted in washed sand.
                The rooted cuttings were maintained for 50 days (May 1
                2003 harvest) under ambient conditions in a local
                greenhouse. They were kept on a weekly regimen of 0.5x

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ORIGIN
Query Match      6.3%; Score 39; DB 8; Length 742;
Best Local Similarity 58.0%; Pred. No. 0.74;
Matches 69; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 275 TTAAGAGTGGGTAGCAGCGGATAGTGAACCGCAAAATGTCGTTTGGGTATCA 334
Db 138 TTAAGAGTGGGTAGCAGCGGATAGTGAACCGCAAAATGTCGTTTGGGTATCA 197
Qy 335 ACATCACCATAAGAAATGACGCGATCCACTCCTATGGAGGTGTTGATGGCATATTTCCAT 393
Db 198 AACAGGGAAGTGACATGTCGTCACACATTAAGGAGCGCGTTAAGGCGAGTCTCCAT 256

RESULT 8
COI67205
LOCUS      FLD1_67_C04_g1_A029 Root flooded Pinus taeda cDNA clone
DEFINITION FLD1_67_C04_g1_A029 5', mRNA sequence.
ACCESSION  COI67205
VERSION     COI67205.1 GI:48937746
KEYWORDS    EST.
SOURCE      Pinus taeda (loblolly pine)
ORGANISM    Pinus taeda
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE   1 (bases 1 to 782)
AUTHORS     Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Zimmermann,C.,
            Johnson,H., Anfuso,C., Kamran,D., Chhabra,D. and Dean,J.F.D.
TITLE       A loblolly pine (Pinus taeda) EST database from flooded roots
JOURNAL     Unpublished (2004)
COMMENT     Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            RNA prepared and library constructed by W. Walter Lorenz (School of
            Forest Resources, University of Georgia); plant material prepared
            by Craig Zimmermann (School of Forest Resources, University of
            Georgia) using rooted cuttings provided by the Forest Biology
            Research Cooperative (FBRC) and the CCLONES project a the
            University of Florida; sequencing done in the Laboratory for
            Genomics and Bioinformatics, University of Georgia. Sequence ends
            have been trimmed to exclude vector and regions below phred quality
            16. Three-prime sequences are presented as their reverse complement
            and have been trimmed to exclude polyA.
            Seq primer: JENREV (CAGAAACAGCTATGACC).
            Location/Qualifiers
                1..782
                /organism="Pinus taeda"
                /mol_type="mRNA"
                /strain="3 CCLONES"
                /db_xref="taxon:3352"
                /clone="FLD1_67_C04_A029"
                /lab_host="DH10B-T1 phage-resistant E. coli"
                /clone_lib="Root flooded"
                /note="Organ: root; Vector: pSL1180; Site 1: ECORI;
                Site 2: XhoI; The library was prepared from polyA+ RNA
                from the roots of 1-year-old loblolly pine (Pinus taeda)
                cuttings that were rooted and then planted in washed sand.
                Prior to harvesting tissues for RNA isolation, the rooted
                cuttings were maintained for 27 days (April 2003) under

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nutrient-complete Hoagland's solution and supplemented
with additional water sufficient to maintain a 15% soil
moisture content. Twenty-four hours (24h) prior to
harvesting roots for mRNA preparation, the potted trees
were placed in a dark growth chamber at 25 C.
Double-stranded cDNA was cloned unidirectionally into
pSL1180. Inserts can be excised with EcoRI (5' end) and
XhoI (3' end)."
```


ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain 5% soil moisture content. Pots holding the rooted cuttings were fully submerged in water for 24 hours prior to harvest of the roots for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts can be excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

| | Query Match | 6.3% | Score 39 | DB 7 | Length 782 | |
|----|-----------------------|----------------|--|----------|------------|--|
| | Best Local Similarity | 58.0% | Pred. No. 0.75 | | | |
| | Matches 69 | Conservative 0 | Mismatches 50 | Indels 0 | Gaps 0 | |
| Qy | 275 | TTAAGAGTG | GGGGTACGACGGGATAGGTGAAACCGCAATGGTGCCTTTGGGGTATCA | 334 | | |
| | | | | | | |
| Db | 284 | TTAAAGTAGG | GATACGTCGGGAAGGGAAGTCTCTTTTGTGCTCTTCAAGGATGCA | 343 | | |
| | | | | | | |
| Qy | 335 | ACATCACCATA | GAAGATGACGGATCCACTCCTATGGAGGTGCTTGTATGGCATATTCAT | 393 | | |
| | | | | | | |
| Db | 344 | AACAGGGAAG | TGACATGTCGTCCCAACAATTAAGGAGGCGCTTAAGGGCAGTCTCCAT | 402 | | |
| | | | | | | |

| | |
|------------|---|
| RESULT 9 | |
| BJ440426/c | |
| LOCUS | 371 bp mRNA linear EST 13-MAR-2002 |
| DEFINITION | BJ440426 Dictyostelium discoideum cDNA library, VF Dictyostelium discoideum cDNA clone ddv43116 3', mRNA sequence. |
| ACCESSION | |
| VERSION | BJ440426 |
| KEYWORDS | BJ440426.1 GI:19415148 |
| SOURCE | EST. |
| ORGANISM | Dictyostelium discoideum |
| | Dictyostelium discoideum |
| | Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium. |
| REFERENCE | 1 (bases 1 to 371) |
| AUTHORS | Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T. |
| TITLE | Full length cDNA of Dictyostelium discoideum at the vegetative |

Unpublished (2002)
Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
Location/Qualifiers
1. .371

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source
1. 374
/organism="Dictyostellium discoideum"
/mol_type="mRNA"
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/db_xref="taxon:44689"
/clone="ddv43116"
/sex="mat A"
/dev_stage="Growth phase"
clone_1b="Dictyostellium discoideum cDNA library. VF"

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| ORIGIN | | /crone_11b- dictyoscellum discordeum cDNA library, v1 | |
|-----------------------|-------|---|----------------------------------|
| Query Match | 6.2% | Score 38.6; | DB 3; Length 371; |
| Best Local Similarity | 51.4% | Pred. No. 0.8; | |
| Matches | 89; | Conservative 0; | Mismatches 84; Indels 0; Gaps 0; |
| Qy | 299 | TAGGTGAACCGCAAAATGGTTCGTTTTGGGTTTATCAACATCACCATGAAGAAATGACGGAT | 358 |
| | | | |
| Db | 252 | TGGTTGAARAAGAAATAAANAAGTTAATGATATCACAAAACCGTATTAGATGTCGAAT | 193 |
| | | | |
| Qy | 359 | CCACTCCTATGGAGGTCGTTGATGGCATAATTCATTTGCAGAACTTAAACGGGAACGTTT | 418 |
| | | | |
| Db | 192 | CTTTTGTTAATGATCACCCAGGTGGTTTACGTTTACATTTAAATTTGGGTATTGGTAAAGATG | 133 |
| | | | |
| Qy | 419 | ATCAGCGGGAATCTCATGCTTGAGATATATGCAAAATACAAATTCAGGGACTTATT | 471 |
| | | | |

| | | | |
|------------|-----|---|----|
| Db | 132 | CAACTTCATGTTTACTGGTGAAGTTTATGCTCAATCAATGCTGCTAAAAAT | 80 |
| RESULT 10 | | | |
| BJ440571/c | | | |
| LOCUS | | | |
| DEFINITION | | | |
| ACCESSION | | | |
| VERSION | | | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | | |
| REFERENCE | | | |
| AUTHORS | | | |
| TITLE | | | |
| JOURNAL | | | |
| COMMENT | | | |
| FEATURES | | | |
| source | | | |

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source
1: 3.3.1
/organism="Dictyostelium discoideum"
/mol_type="mrna"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddv44i05"
/sex="mat A"
/dev_stage="Growth phase"
/clone_lib="Dictyostelium discoideum cDNA library, VF"
ORIGIN

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| | Query Match | 6.2% | Score 38.6; | DB 3; | Length 374; |
|----|-----------------------|---|----------------|-----------|-------------|
| | Best Local Similarity | 51.4%; | Pred. No. 0.8; | | |
| | Matches 89; | Conservative 0; | Mismatches 84; | Indels 0; | Gaps 0; |
| Qy | 299 | TAGGTGAACCGCAAAATGGTGGCTTTTGGGTATCAACATCACCATAAGCAATGACGGAT | 358 | | |
| Db | 256 | TGGTTGAAAAGAAGAAATAAAAAGTTAATGATAATCAACAAAACCGTATTAGATGTGCAAT | 197 | | |
| Qy | 359 | CCACTCTATGGAGGTCGTTGATGGCATATTCATTTCAGAGACTTTAAACGGGAACGTTT | 418 | | |
| Db | 196 | CTTTGTTAATGATACACCGAGTGGTTTAGCTTACATTAAATGGGTATTGGTAAAGATG | 137 | | |
| Qy | 419 | ATCAGCGCGGATTTCTACTGCTGAGATATATGCAAAATACAAATTCAGGGACTATT | 471 | | |
| Db | 136 | CAACCTTCAGAGTTTATCTGGTGAAGTTTATGCTCATTTCTCAATGCTGTCTAAAAAT | 84 | | |

[illegible]

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1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers

FEATURES

source
1. .391
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddv44m07"
/sex="mat A"
/dev_stage="Growth phase"
/clone_lib="Dictyostelium discoideum cDNA library, VF"

ORIGIN

Query Match 6.2%; Score 38.6; DB 3; Length 391;
Best Local Similarity 51.4%; Pred. No. 0.81;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 299 TAGGTGAACCGCAAAATGGTGGCTTATGAGTATCAACATCACCATAAGAAATGACGGAT 358
Db 248 TGGTTGAAAAAGAAAATAAAAAAGTTAATGATAATCAACAAAACCGTATTAGATGTCGAAT 189
Qy 359 CCACCTCCTATGGAGGTGGTTGATGGCATATTCATTTGCAGAACTTAAACGGGAACGTTT 418
Db 188 CTTTGTGTTAATGATCACCAGGTGGTTAGCTTACATTAATAATGGGTATTGGTAAAGATG 129
Qy 419 ATCAGCGGGATTCCTACTGCTGAGATATATGCAAAATCAAAATTCAGGGACTATT 471
Db 128 CAACTTCAATGTTTACTGGTGAAGTTTATGCTCATTCATCAATGCTGCTAAAAAT 76

RESULT 12
BJ440820/c
LOCUS
DEFINITION BJ440820 Dictyostelium discoideum cDNA library, VF Dictyostelium
discoideum cDNA clone ddv44g24 3', mRNA sequence.
ACCESSION BJ440820.1 GI:19415542
VERSION
KEYWORDS
SOURCE
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
REFERENCE 1 (bases 1 to 393)
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE Full length cDNA of Dictyostelium discoideum at the vegetative stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers

FEATURES

source
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Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 299 TAGGTGAACCGCAAAATGGTGGCTTATGAGTATCAACATCACCATAAGAAATGACGGAT 358
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Qy 359 CCACCTCCTATGGAGGTGGTTGATGGCATATTCATTTGCAGAACTTAAACGGGAACGTTT 418
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Qy 419 ATCAGCGGGATTCCTACTGCTGAGATATATGCAAAATCAAAATTCAGGGACTATT 471
Db 128 CAACTTCAATGTTTACTGGTGAAGTTTATGCTCATTCATCAATGCTGCTAAAAAT 76

RESULT 13

BJ440720/c
LOCUS
DEFINITION BJ440720 Dictyostelium discoideum cDNA library, VF Dictyostelium
discoideum cDNA clone ddv44d15 3', mRNA sequence.
ACCESSION BJ440720
VERSION BJ440720.1 GI:19415442
KEYWORDS
SOURCE
ORGANISM Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
REFERENCE 1 (bases 1 to 394)
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE Full length cDNA of Dictyostelium discoideum at the vegetative stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers

FEATURES

source
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ORIGIN

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Best Local Similarity 51.4%; Pred. No. 0.81;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 299 TAGGTGAACCGCAAAATGGTGGCTTATGAGTATCAACATCACCATAAGAAATGACGGAT 358
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Db 193 CTTTGTGTTAATGATCACCAGGTGGTTAGCTTACATTAATAATGGGTATTGGTAAAGATG 134
Qy 419 ATCAGCGGGATTCCTACTGCTGAGATATATGCAAAATCAAAATTCAGGGACTATT 471
Db 133 CAACTTCAATGTTTACTGGTGAAGTTTATGCTCATTCATCAATGCTGCTAAAAAT 81

RESULT 14

BJ437922/c
LOCUS
DEFINITION BJ437922 Dictyostelium discoideum cDNA library, VF Dictyostelium
discoideum cDNA clone ddv35e19 3', mRNA sequence.
ACCESSION BJ437922
VERSION BJ437922.1 GI:19412644
KEYWORDS

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SOURCE      Dictyostelium discoideum
ORGANISM    Dictyostelium discoideum
REFERENCE   1 (bases 1 to 422)
AUTHORS     Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE       Full length cDNA of Dictyostelium discoideum at the vegetative
            stage
JOURNAL     Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
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               /sex="mat A"
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               /clone_lib="Dictyostelium discoideum cDNA library, VF"
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Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
Qy 299 TAGGTGAACCGCAAAATGGTGGCTTTGGGTTATCAACATCACCATAAGAATGACGGAT 358
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Qy 359 CCACCTCCATGAGGTCGTTCATGTCATATTCCTTTCAGAACTTAAACGGGAACGTTT 418
Db 187 CTTTGTGTTAATGATCACCAGGTGGTTTAGCTTACATTAAATGGGTATTGGTAAAGATG 128
Qy 419 ATCAGCGCGATTCTACTGCTGAGATATATGCAAAATACAAATTCAGGGACTATT 471
Db 127 CAACTTCAATGTTTACTGGTGAAGTTTATGCTCATTCAATGCTGCTAAAAAT 75

RESULT 15
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LOCUS      458 bp mRNA linear EST 13-MAR-2002
DEFINITION BJ444052 Dictyostelium discoideum cDNA library, VF Dictyostelium
            discoideum cDNA clone ddv55f06 3', mRNA sequence.
ACCESSION  BJ444052.1 GI:19418773
VERSION    BJ444052
KEYWORDS   EST.
SOURCE     Dictyostelium discoideum
ORGANISM   Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1 (bases 1 to 458)
AUTHORS     Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE       Full length cDNA of Dictyostelium discoideum at the vegetative
            stage
JOURNAL     Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES    source
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               /mol_type="mRNA"
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/sex="mat A"
/dev_stage="Growth phase"
/clone_lib="Dictyostelium discoideum cDNA library, VF"
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Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
Qy 299 TAGGTGAACCGCAAAATGGTGGCTTTGGGTTATCAACATCACCATAAGAATGACGGAT 358
Db 254 TGGTTGAAAAAGAAAAAAGTTAATGATAATCAACAAAACCGTATTAGATGTCGAAT 195
Qy 359 CCACCTCCATGAGGTCGTTCATGTCATATTCCTTTCAGAACTTAAACGGGAACGTTT 418
Db 194 CTTTGTGTTAATGATCACCAGGTGGTTTAGCTTACATTAAATGGGTATTGGTAAAGATG 135
Qy 419 ATCAGCGCGATTCTACTGCTGAGATATATGCAAAATACAAATTCAGGGACTATT 471
Db 134 CAACTTCAATGTTTACTGGTGAAGTTTATGCTCATTCAATGCTGCTAAAAAT 82

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 33.8 | 5.4 | 181251 | 3 | US-09-949-016-15970 |
| 3 | 33.4 | 5.4 | 421118 | 3 | US-09-949-016-16297 |
| 4 | 32.4 | 5.2 | 285478 | 3 | US-09-949-016-13362 |
| 5 | 32.2 | 5.2 | 1141 | 3 | US-09-806-708B-22 |
| 6 | 32 | 5.2 | 832 | 3 | US-09-621-976-2813 |
| 7 | 32 | 5.2 | 99304 | 3 | US-09-949-016-15440 |
| 8 | 31.4 | 5.1 | 17000 | 3 | US-09-679-299A-18 |
| 9 | 31.4 | 5.1 | 236964 | 3 | US-09-949-016-15753 |
| 10 | 31.2 | 5.0 | 8439 | 3 | US-09-221-017B-473 |
| 11 | 30.8 | 5.0 | 1995 | 3 | US-09-710-279-1257 |
| 12 | 30.8 | 5.0 | 2169 | 3 | US-09-134-001C-2645 |
| 13 | 30.8 | 5.0 | 3356 | 3 | US-09-710-279-3920 |
| 14 | 30.6 | 4.9 | 3001 | 3 | US-09-539-333D-185 |
| 15 | 30.4 | 4.9 | 601 | 3 | US-09-949-016-151347 |
| 16 | 30.4 | 4.9 | 601 | 3 | US-09-949-016-151410 |
| 17 | 30.4 | 4.9 | 3509 | 3 | US-09-949-016-4254 |
| 18 | 30.4 | 4.9 | 3509 | 3 | US-09-949-016-4255 |
| 19 | 30.4 | 4.9 | 118382 | 3 | US-09-949-016-15996 |
| 20 | 30.4 | 4.9 | 118382 | 3 | US-09-949-016-15997 |
| 21 | 30.2 | 4.9 | 1194 | 3 | US-09-270-767-5598 |
| 22 | 30.2 | 4.9 | 1194 | 3 | US-09-270-767-20880 |
| 23 | 30 | 4.8 | 601 | 3 | US-09-949-016-128577 |
| 24 | 30 | 4.8 | 601 | 3 | US-09-949-016-128578 |

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| 25 | 30 | 4.8 | 601 | 3 | US-09-949-016-150405 | Sequence 150405, |
| c 26 | 30 | 4.8 | 1270 | 3 | US-09-415-277C-1 | Sequence 1, Appli |
| c 27 | 30 | 4.8 | 1270 | 3 | US-09-415-277C-16 | Sequence 16, Appli |
| c 28 | 30 | 4.8 | 1271 | 3 | US-09-415-277C-3 | Sequence 3, Appli |
| 29 | 30 | 4.8 | 24205 | 3 | US-09-949-016-15385 | Sequence 15385, A |
| 30 | 29.8 | 4.8 | 351 | 3 | US-09-248-796A-2992 | Sequence 2992, Ap |
| 31 | 29.8 | 4.8 | 947 | 3 | US-09-640-211A-138 | Sequence 138, App |
| 32 | 29.8 | 4.8 | 1164 | 3 | US-09-248-796A-4125 | Sequence 4125, Ap |
| 33 | 29.8 | 4.8 | 1443 | 3 | US-09-248-796A-668 | Sequence 668, App |
| 34 | 29.8 | 4.8 | 2090 | 3 | US-09-270-767-4280 | Sequence 4280, Ap |
| 35 | 29.8 | 4.8 | 2090 | 3 | US-09-270-767-19562 | Sequence 19562, A |
| 36 | 29.8 | 4.8 | 5619 | 3 | US-09-799-451-241 | Sequence 241, App |
| 37 | 29.8 | 4.8 | 319608 | 3 | US-09-539-333D-1 | Sequence 1, Appli |
| c 38 | 29.6 | 4.8 | 601 | 3 | US-09-949-016-102623 | Sequence 102623, |
| c 39 | 29.6 | 4.8 | 601 | 3 | US-09-949-016-102735 | Sequence 102735, |
| c 40 | 29.6 | 4.8 | 601 | 3 | US-09-949-016-128576 | Sequence 128576, |
| c 41 | 29.6 | 4.8 | 7917 | 2 | US-08-167-854-1 | Sequence 1, Appli |
| 42 | 29.6 | 4.8 | 678533 | 3 | US-09-949-016-14577 | Sequence 14577, A |
| 43 | 29.6 | 4.8 | 678533 | 3 | US-09-949-016-14578 | Sequence 14578, A |
| c 44 | 29.4 | 4.7 | 601 | 3 | US-09-949-016-131570 | Sequence 131570, |
| 45 | 29.4 | 4.7 | 1211 | 3 | US-08-858-207A-128 | Sequence 128, App |

ALIGNMENTS

RESULT 1

US-09-949-016-150404
; Sequence 150404, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150404
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150404

Query Match 5.4%; Score 33.8; DB 3; Length 601;
Best Local Similarity 52.5%; Pred. No. 0.57;
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

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| Qy | 63 | TTCTTTGGTTAAATTCGACGAATAGTTCACAGGTAGCAAGCAAGCAAACTCGAGTAC | 122 |
| Db | 131 | TTTTTTTTTCAGTGGGTCTATTTTTTAAATGTAATAGCATAACATAAAATTTACTAT | 190 |
| Qy | 123 | GTCTCCCGCTCATAGTCTAGCAACTCATTTGCAACATCGGCAACATCAAGTGTCTACGAC | 182 |
| Db | 191 | TTTAAACAATTTTTAAAGTGTACAGTAGCATTTACACATTTTACATCATTTGTGCGCTGTAC | 250 |
| Qy | 183 | TTCATCTTCTTCAGTCGAAGTT | 203 |
| Db | 251 | TACCATCCATCTCTAGAACTT | 271 |

RESULT 2

US-09-949-016-15970
; Sequence 15970, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15970
; LENGTH: 181251
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15970

Query Match      5.4%; Score 33.8; DB 3; Length 181251;
Best Local Similarity 52.5%; Pred. No. 7.9;
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy      63  TTCTTTGGTTAAATTCGACGAATAGTTCACAGGTAGCAAGCAAGCAAACTCGAGTAC 122
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Qy      123  GTCTCCCGCTCATAGTCTACGAACTCATGCAACATGCGCAACATCAAGTGTACGAC 182
Db      58750  TTTTAAACAATTTTAAAGTGTACAGTAGCATTAACAACATTTACATCATGTGCGAGCTGTAC 58809

Qy      183  TTCACTCTCTCAGTCGAAGTT 203
Db      58810  TACCATCCATCTCTAGAAGTT 58830

RESULT 3
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; Sequence 16297, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16297
; LENGTH: 421118
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(421118)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16297

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Best Local Similarity 49.2%; Pred. No. 16;
Matches 88; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy      381  TGGCATATTCATTTGCAAGACTTAAACGGGAAGCTTTTATCAGCGGATTTCTACTGTGA 440
Db      264214  TAGAATCCATCATTTGTGTAACAAATAACGGCATGTTTTCACAAAAGGATTTGACTTTTCA 264155
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Qy      441  GATATATGCAAAATACAAATTCAGGACTATTCGACCGAGCTCAACCCCTGGTGTGTCAT 500
Db      264154  GGTATTTTCTATTTATTTGCTGAAGCTAGATTAGAAAGCTAACTCTAGTATCCTGGGTATTA 264095

Qy      501  GACGACAAATCTCGTATTTGATATGCGGATTTTATGACATATGTTACATCGTGGGCGAGC 559
Db      264094  CATTACGAGGAGGCTTTGAAAATTTGAAAATTTTCCACACATGGGATGTTATGGTAGC 264036

RESULT 4
US-09-949-016-13362
; Sequence 13362, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13362
; LENGTH: 285478
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(285478)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13362

Query Match      5.2%; Score 32.4; DB 3; Length 285478;
Best Local Similarity 58.2%; Pred. No. 29;
Matches 57; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy      126  TCCCGCTCATAGTCTACGAACTCATGCAACATGCGCAACATCAAGCTGTACGACTTC 185
Db      35275  TCTCCCTCTCAGCCTCTTAAGTATCTGGAACGTGCGCCACACACCCCGGCTAAGTTTT 35334

Qy      186  ATCTTCTCAGTCGAAGTTACGATATATCCCGTTTCA 223
Db      35335  GTATTTTCGGTAGAGATGGGGTTTCACCATGTTGCCCA 35372

RESULT 5
US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)...(1141)
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Qy 375 CGTTGATGGCATATTCATT 394
Db 5306 CTATGCCGGCATTTGCTACT 5325

RESULT 11
US-09-710-279-1257/c
; Sequence 1257, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1257
; LENGTH: 1995
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-1257

Query Match 5.0%; Score 30.8; DB 3; Length 1995;
Best Local Similarity 52.3%; Pred. No. 10;
Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 150 ATTGCAACATCGGCAACATCAAGCTGTACGACTTCATCTTCTCAGTCGAAGTTACGATA 209
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Db 263 ATTGCGAGTCTGATTATTAATCTCTCAAGAACTAGTTTATCATTCGTTTTTAAAGCG 204
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Qy 210 TATCCCGTTTCACATACGCGAAGGTAGGAGACTTGGAAATTAGCTTAAGTTACTCCCTGCA 269
Db 203 TAATCCTTTATAAACTTACTTGGCAGACATATACTAGCAAAATTGGAAGTGAATTGATTTT 144
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Qy 270 GCAAGTTAAG 279
Db 143 GCGTATTCAG 134
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RESULT 12
US-09-134-001C-2645/c
; Sequence 2645, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2645
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2645

Query Match 5.0%; Score 30.8; DB 3; Length 2169;
Best Local Similarity 52.3%; Pred. No. 11;
Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 150 ATTGCAACATCGGCAACATCAAGCTGTACGACTTCATCTTCTCAGTCGAAGTTACGATA 209
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Db 437 ATTGCGAGTCTGATTATTAATCTCAAGAACTAGTTTTTATCATTCGTTTTTAAAGCG 378
Qy 210 TATCCCGTTTCACACATACGCGAAGGTAGGAGACTTGGAAATTAGAGTTAACTCCCTGCA 269
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Db 377 TAATCCTTTATAAACTTACTTGGCAGACATATACTAGCAAAATTGGAAGTGAATTGATTTT 318
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Qy 270 GCAAGTTAAG 279
Db 317 GCGTATTCAG 308
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RESULT 13
US-09-710-279-3920/c
; Sequence 3920, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3920
; LENGTH: 3356
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3920

Query Match 5.0%; Score 30.8; DB 3; Length 3356;
Best Local Similarity 52.3%; Pred. No. 13;
Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 150 ATTGCAACATCGGCAACATCAAGCTGTACGACTTCATCTTCTCAGTCGAAGTTACGATA 209
|||||
Db 666 ATTGCGAGTCTGATTATTAATCTCTCAAGAACTAGTTTTTATCATTCGTTTTTAAAGCG 607
|||||

Qy 210 TATCCCGTTTCACACATACGCGAAGGTAGGAGACTTGGAAATTAGAGTTAACTCCCTGCA 269
Db 606 TAATCCTTTATAAACTTACTTGGCAGACATATACTAGCAAAATTGGAAGTGAATTGATTTT 547
|||||

Qy 270 GCAAGTTAAG 279
Db 546 GCGTATTCAG 537
|||||

RESULT 14
US-09-539-333D-185
; Sequence 185, Application US/09539333D
; Patent No. 8476208
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Bessieux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: GENSET.047AUS
; CURRENT APPLICATION NUMBER: US/09/539,333D
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928

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; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/416,384
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent.pm
; SEQ ID NO 185
; LENGTH: 3001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1501
; OTHER INFORMATION: 99-25917-115 : polymorphic base G or A
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 1502..1520
; OTHER INFORMATION: 99-25917-115.mis1, complement
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 1481..1500
; OTHER INFORMATION: 99-25917-115.mis2,
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 1595..1615
; OTHER INFORMATION: upstream amplification primer, complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1115..1135
; OTHER INFORMATION: downstream amplification primer
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 1489..1513
; OTHER INFORMATION: 99-25917-115 probe
US-09-539-333D-185

Query Match          4.9%; Score 30.6; DB 3; Length 3001;
Best Local Similarity 62.3%; Pred. No. 14;
Matches 48; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy      299 TAGGTGAACCGCAAAATGGTCGTTTGGGTTATCAACATCACCATAGAAATGACCGAT 358
Db      1276 TAAAGTAAACACAGATGTTCTTTTGTCTGATCAAAATGAAATAGGGACTATAGTT 1335

Qy      359 CCACCTCTATGAGGTC 375
Db      1336 CCACTTCTTTGAGCTC 1352

RESULT 15
US-09-949-016-151347/c
; Sequence 151347, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151347
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-151347

Query Match          4.9%; Score 30.4; DB 3; Length 601;
Best Local Similarity 50.7%; Pred. No. 8.1;
Matches 73; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy      395 TGCAGAACTTAAACGGGAAGCTTTATCAGCCGGATTCTACTGCTGAGATATATGCAATA 454
Db      145 TTCAGAGTAGCTCAGCGAGGAAGCAGTTGCAATTGTACTTTGAAGATAAAGTCAACA 86

Qy      455 CAAATTCAGGGACTATTTCGACCGACCTCAACCTGGTGTGTCATGACGACAAATCTCG 514
Db      85 GATCTACTCAGACAGGACCTTCGCACCTTTGCCAGAGTTTGACGAGGAGGATGATGG 26

Qy      515 TATTTGATATGCCGGATTTTATGA 538
Db      25 TGAGGTAAGTGAAGACTCTGATGA 2

Search completed: April 12, 2006, 08:21:09
Job time : 176 secs
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GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM nucleic - nucleic search, using sw model
 Run on: April 12, 2006, 07:48:54 ; Search time 798 Seconds
 (without alignments)
 6435.193 Million cell updates/sec

Title: US-10-784-592-18_COPY_124_744
 Perfect score: 621
 Sequence: 1 aacacgtgtatgatcg.....aaacagcatgtcttcttcg 621

Scoring table: IDENTITY_NUC
 Gapop 10.0 ; Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:
 1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq.*
 2: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq.*
 3: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq.*
 4: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq.*
 5: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq.*
 6: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq.*
 7: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq.*
 8: /cgn2_6/ptodata/1/pubna/US10D_PUBCOMB.seq.*
 9: /cgn2_6/ptodata/1/pubna/US10E_PUBCOMB.seq.*
 10: /cgn2_6/ptodata/1/pubna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-----------------------|
| 1 | 621 | 100.0 | 744 | 9 | US-10-784-592-18 |
| 2 | 35.2 | 5.7 | 580 | 9 | US-10-487-901-4181 |
| 3 | 35 | 5.6 | 2349 | 6 | US-10-369-493-37301 |
| 4 | 34.4 | 5.5 | 4818 | 7 | US-10-437-963-69024 |
| 5 | 34.2 | 5.5 | 1502 | 4 | US-09-925-065A-429103 |
| 6 | 33.8 | 5.4 | 591 | 4 | US-09-925-065A-429103 |
| 7 | 33.8 | 5.4 | 660 | 8 | US-10-425-115-125681 |
| 8 | 33.8 | 5.4 | 729 | 7 | US-10-425-114-6745 |
| 9 | 33.8 | 5.4 | 860 | 7 | US-10-425-114-6834 |
| 10 | 33.8 | 5.4 | 935 | 8 | US-10-425-115-154424 |
| 11 | 33.8 | 5.4 | 1240 | 4 | US-09-925-065A-41609 |
| 12 | 33.4 | 5.4 | 706 | 9 | US-10-487-901-3702 |
| 13 | 33.4 | 5.4 | 1048 | 7 | US-10-767-701-11172 |
| 14 | 33.2 | 5.3 | 534 | 4 | US-09-925-065A-427028 |
| 15 | 32.8 | 5.3 | 641 | 4 | US-09-925-065A-178736 |
| 16 | 32.6 | 5.2 | 566 | 4 | US-09-925-065A-604703 |
| 17 | 32.6 | 5.2 | 566 | 4 | US-09-925-065A-604704 |
| 18 | 32.6 | 5.2 | 2700 | 7 | US-10-683-516-4 |
| 19 | 32.4 | 5.2 | 611 | 4 | US-09-925-065A-760902 |
| 20 | 32.4 | 5.2 | 813 | 7 | US-10-283-122A-16587 |
| 21 | 32.4 | 5.2 | 301477 | 7 | US-10-322-281-456 |
| 22 | 32.2 | 5.2 | 598 | 4 | US-09-925-065A-301137 |
| 23 | 32.2 | 5.2 | 123526 | 3 | US-09-910-185-11 |

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24      32      5.2      1470      7      US-10-437-963-89649      Sequence 89649, A
25      32      5.2      26147      10      US-11-097-143-14227      Sequence 14227, A
26      31.8      5.1      533      4      US-09-925-065A-413580      Sequence 413580,
c 27      31.8      5.1      534      6      US-10-264-049-1203      Sequence 1203, Ap
c 28      31.8      5.1      573      4      US-09-925-065A-429103      Sequence 429103,
c 29      31.8      5.1      615      4      US-09-925-065A-517010      Sequence 517010,
c 30      31.8      5.1      383432      9      US-10-737-082-34      Sequence 34, Appl
c 31      31.8      5.1      383432      9      US-10-765-790-34      Sequence 34, Appl
c 32      31.6      5.1      323      6      US-10-063-685-126      Sequence 126, App
c 33      31.6      5.1      704      9      US-10-487-901-6016      Sequence 6016, Ap
c 34      31.6      5.1      1007      9      US-10-487-901-4206      Sequence 4206, Ap
c 35      31.6      5.1      1394      4      US-09-925-065A-71186      Sequence 71186, A
c 36      31.4      5.1      501      7      US-10-424-599-11847      Sequence 11847, A
c 37      31.4      5.1      540      4      US-09-925-065A-747461      Sequence 747461,
c 38      31.4      5.1      545      4      US-09-925-065A-746148      Sequence 746148,
c 39      31.4      5.1      567      5      US-10-027-632-139918      Sequence 139918,
c 40      31.4      5.1      567      6      US-10-027-632-139918      Sequence 139918,
c 41      31.4      5.1      611      4      US-09-925-065A-226317      Sequence 226317,
c 42      31.4      5.1      709      7      US-10-767-701-8345      Sequence 8345, Ap
c 43      31.4      5.1      735      5      US-10-184-644-88      Sequence 88, Appl
c 44      31.4      5.1      735      5      US-10-184-634-88      Sequence 88, Appl
c 45      31.4      5.1      1033      7      US-10-437-963-14402      Sequence 14402, A

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ALIGNMENTS

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RESULT 1
US-10-784-592-18
; Sequence 18, Application US/10784592
; Publication No. US20050147983A1
; GENERAL INFORMATION:
; APPLICANT: Wilting, Reinhard
; APPLICANT: Ostergaard, Peter
; APPLICANT: Lassen, Soren
; TITLE OF INVENTION: POLYPEPTIDES OF ALICYCLOBACILLUS SP.
; FILE REFERENCE: 10406.203-US
; CURRENT APPLICATION NUMBER: US/10/784.592
; CURRENT FILING DATE: 2004-02-23
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Alicyclobacillus sp.
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: (1)..(744)
; OTHER INFORMATION: CDS
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(123)
; OTHER INFORMATION: sig_peptide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (124)..(744)
; OTHER INFORMATION: mat_peptide
US-10-784-592-18

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Query Match      100.0%; Score 621; DB 9; Length 744;
Best Local Similarity 100.0%; Pred. No. 2.1e-201;
Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AACACGGTGTATGATTTCGAGGAAACACACCGGGGAACGCATCAACGGTAAAGCGCTACA 60
      |||
Db      124 AACACGGTGTATGATTTCGAGGAAACACACCGGGGAACGCATCAACGGTAAAGCGCTACA 183
QY      61 ACTTCTTTGGTTAATTCGACGAATAGTTCACAGGTAGCAAGCAAGCAAACTCGAGT 120
      |||
Db      184 ACTTCTTTGGTTAATTCGACGAATAGTTCACAGGTAGCAAGCAAGCAAACTCGAGT 243
QY      121 ACCTCTCCGCTCATAGTCTACCACTTCGCAACATGCGCAACATCAAGCTGCTACG 180
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Db 244 ACGTCTCCGCTCATAGTCTACGAAGCTATTGCAACATGCGCAACATCAAGCTGCTACG 303
Qy 181 ACTTCATCTTCTCAGTGAAGTTAGGATATATCCGTTTTCACATACGGAAGGTAGGA 240
Db 304 ACTTCATCTTCTCAGTGAAGTTAGGATATATCCGTTTTCACATACGGAAGGTAGGA 363
Qy 241 GACTTGGAAATTAGAGTTAACTCCCTCGCAGCAAGTTAAGAGTGTGGGTACGCGGGATA 300
Db 364 GACTTGGAAATTAGAGTTAACTCCCTCGCAGCAAGTTAAGAGTGTGGGTACGCGGGATA 423
Qy 301 GGTGAACCGCAATGGTGGCTTTTGGGTTATCAACATCACCATTAAGAAATGACGGATCC 360
Db 424 GGTGAACCGCAATGGTGGCTTTTGGGTTATCAACATCACCATTAAGAAATGACGGATCC 483
Qy 361 ACTCCTATGAGAGTGGTGGATATTCATTTGAGAACTTAAACGGGAAGCTTTAT 420
Db 484 ACTCCTATGAGAGTGGTGGATATTCATTTGAGAACTTAAACGGGAAGCTTTAT 543
Qy 421 CAGCGGATTTCTACTGCTGAGATATATGCAAAATTCAGGAGCTATTTCGACCGAC 480
Db 544 CAGCGGATTTCTACTGCTGAGATATATGCAAAATTCAGGAGCTATTTCGACCGAC 603
Qy 481 CTCAACCTGCTGTGTCATGACGACAAATCTCGTATTGATATGCCGATTTTATGACA 540
Db 604 CTCAACCTGCTGTGTCATGACGACAAATCTCGTATTGATATGCCGATTTTATGACA 663
Qy 541 TATGGTCACTGCGGGAGCATTAATCTGCTGCTTCCATGGGTTTCTCGGTCAGAT 600
Db 664 TATGGTCACTGCGGGAGCATTAATCTGCTGCTTCCATGGGTTTCTCGGTCAGAT 723
Qy 601 GAAACGACGTATGCTCTTCCG 621
Db 724 GAAACGACGTATGCTCTTCCG 744

RESULT 2

US-10-487-901-4181/c
; Sequence 4181, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larriua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4181
; LENGTH: 580
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-4181

Query Match 5.7%; Score 35.2; DB 9; Length 580;
Best Local Similarity 53.7%; Pred. No. 1;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
Qy 325 TGGGTATCAACATCACCATTAAGAAATGACGGATCCATCTCTATGGAGTTCGTTGATGCG 384
Db 194 TGGGATGACTAGCTTTCCTTAAACGAGCTGAAACCACTACTTTGTAGGCCCTTGATTGC 135

Qy 385 ATATTCATTTCGAGAACTTAAACGGGAACGTTTATCAGCGGATTTCTACTGCTGAGATA 444
Db 134 TTCTTCTTTTCCGAACTACATAATGACCGTCTCTCTGCAAGCTGCGAAGAGAGAT 75
Qy 445 TATGCAAAATCAAAATT 460
Db 74 TGAAGCAACACAAATT 59

RESULT 3

US-10-369-493-37301
; Sequence 37301, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 37301
; LENGTH: 2349
; TYPE: DNA
; ORGANISM: Thermoplasma volcanium
US-10-369-493-37301

Query Match 5.6%; Score 35; DB 6; Length 2349;
Best Local Similarity 55.3%; Pred. No. 2.6;
Matches 68; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 292 GACGGATAGTGAACCGCAAAATGTCGTTTGGGTTTATCAACATCACCATTAAGAAAT 351
Db 1330 GACGGGACAAAGTGGAAACACGGAGTGGCCCAATCCGCTCACCATTAACAAAAAGGC 1389
Qy 352 GACGGATCCCACTCCTATGAGAGTTCGTTGATGGCATATTTCCATTTGCGAACTTAAACGGG 411
Db 1390 AAGTATCTATGCTTAATGGAGGATGAAGTGTACATAGCAAGAAATGCTCAAACTAAACGCA 1449
Qy 412 AAC 414
Db 1450 AAC 1452

RESULT 4

US-10-437-963-69024
; Sequence 69024, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 69024
; LENGTH: 4818
; TYPE: DNA
; ORGANISM: Oryza sativa

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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_69732C.1
US-10-437-963-69024

Query Match      5.5%; Score 34.4; DB 7; Length 4818;
Best Local Similarity 50.0%; Pred. No. 6.2;
Matches 86; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 435 TGCTGAGATATATCAAAATACAAATTCAGGACATATCCGACCGCACTCAACCTGTGTGT 494
Db 939 TACTGAATAGCTAGAAAGGAAAGGCGCGGAATATTAACCTGACCCAGATCTTGATGT 998
QY 495 GTCCATCAGCAGCAAAATCTCGTATTTTATATATCCCGGATTTTATGACATATGTCACGTCGG 554
Db 999 TTACATGAGGCATATCATAGTGGGTGTCAGGAGACAAATATCATCACTGATTAAGTCCT 1058
QY 555 GCAGCATTAATCACTTCCTCGCTCCATCGGTTTCTTCGGGTTCAGATGAAACG 606
Db 1059 CAAGATTCAGGACTTGACATTTTGGCTGACACCAATTTGTTGGAATGAAATG 1110

RESULT 5
US-09-925-065A-724617/c
; Sequence 724617, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 724617
; LENGTH: 1502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-724617

Query Match      5.5%; Score 34.2; DB 4; Length 1502;
Best Local Similarity 45.6%; Pred. No. 3.8;
Matches 120; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 197 CGAAGTTACGATATATCCGTTTTCACATACGCGAAGGTAGGACCTTGGAAATTAGAG 256
Db 783 CTAATGTAGGAGCATTTCTGGCATGCTCAAAGACAGCAAGAGACCTGTGTGGATAGAG 724
QY 257 TTAATCCCTGCAGCAAGTTAAGAGTGTGGGTACGACGGATAGGTGAAACCGCAATG 316
Db 723 TGAAGTGGATGGGTGTGGAAGGAAGAGTAGTATATGTTAAGAGATGTACAGGAGTC 664
QY 317 GTGCGTTTGGGTTATCAACATCAACCAATGACCGATCCACCTCCTATGAGGTCG 376
Db 663 AGATAATTAGGCTTTTGAAGCCACCATAGAAATTTTGGCTTTTCTTCAAGTTATATAG 604
QY 377 TTGATGGCATATTCATTTTCAGAACTTAACGGGAACGTTTATCAGCCGATTTCTACTG 436
Db 603 AAGAAGAATATTCAAATTTTAACTTTTCTGTGCATGAATTTAATAAAGAAATACATGA 544
QY 437 CTGAGATATATGCAATCAAT 459
Db 543 AAATGAAATGTACATCTCAATAT 521
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RESULT 6

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US-09-925-065A-867215
; Sequence 867215, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 867215
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-867215
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Query Match      5.4%; Score 33.8; DB 4; Length 591;
Best Local Similarity 52.5%; Pred. No. 3.1;
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 63 TTCTTTGGTTAATTCGACGATAGTTTCACAGGTAGCAAGCAAGCAAACTCGAGTAC 122
Db 289 TTTTITTTTGGTGGGTCTATTTTAAATTTAAATAGCATTAACATAAAATTTACTAT 348
QY 123 GTCTCCGCTCATAAAGTCTACGAACCTCATTCGAACATCGCAACATCGCAACATCAAGCTGTACGAC 182
Db 349 TTTAAACAATTTTAAAGGTACAGTAGCATTAACATTTTACATCATTTGTGCGAGCTGTAC 408
QY 183 TTCACTCTTCAGTCGAAGTT 203
Db 409 TACCATCCATCTCTAGAAGTT 429
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RESULT 7

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US-10-425-115-125681
; Sequence 125681, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 39-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 125681
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_46091C.1
US-10-425-115-125681
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Query Match      5.4%; Score 33.8; DB 8; Length 660;
Best Local Similarity 52.5%; Pred. No. 3.3;
```

```
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 461 CAGGGACTATTCCGACCGACCTCAACCTGGTGTGTCATGACGACAAATCTCGTATTG 520
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 391 CTGGGCATATGACCGGAGTCAAGCCCAAGGAGTCCAAACGATGTTTAGGAAATGGG 450
QY 521 ATATGCCGGATTTTATGACATATGGTCAAGTCCGGCAGCATTTACTCACTTGTGCTTCCA 580
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 451 TTTCACGGGATCCTCTCTGATATTACGTGCTCTGAGAGAATTACGTACGTGCTGCTCCTA 510
QY 581 TGGGTTTCTTCGGGTACAGT 601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 511 TGAGTGTAGCCGACGTACG 531

RESULT 8
US-10-425-114-6745
; Sequence 6745, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6745
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700577561_FLI
US-10-425-114-6745

Query Match 5.4%; Score 33.8; DB 7; Length 729;
Best Local Similarity 52.5%; Pred. No. 3.5;
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 461 CAGGGACTATTCCGACCGACCTCAACCTGGTGTGTCATGACGACAAATCTCGTATTG 520
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 464 CTGGGCATATGACCGGAGTCAAGCCCAAGGAGTCCAAACGATGTTTAGGAAATGGG 523
QY 521 ATATGCCGGATTTTATGACATATGGTCAAGTCCGGCAGCATTTACTCACTTGTGCTTCCA 580
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 524 TTTCACGGGATCCTCTCTGATATTACGTGCTCTGAGAGAATTACGTACGTGCTGCTCCTA 583
QY 581 TGGGTTTCTTCGGGTACAGT 601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 584 TGAGTGTAGCCGACGTACG 604

RESULT 9
US-10-425-114-6834
; Sequence 6834, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
```

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; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6834
; LENGTH: 860
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700579892_FLI
US-10-425-114-6834

Query Match 5.4%; Score 33.8; DB 7; Length 860;
Best Local Similarity 52.5%; Pred. No. 3.8;
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 461 CAGGGACTATTCCGACCGACCTCAACCTGGTGTGTCATGACGACAAATCTCGTATTG 520
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 600 CTGGGCATATGACCGGAGTCAAGCCCAAGGAGTCCAAACGATGTTTAGGAAATGGG 659
QY 521 ATATGCCGGATTTTATGACATATGGTCAAGTCCGGCAGCATTTACTCACTTGTGCTTCCA 580
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 660 TTTCACGGGATCCTCTCTGATATTACGTGCTCTGAGAGAATTACGTACGTGCTGCTCCTA 719
QY 581 TGGGTTTCTTCGGGTACAGT 601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 720 TGAGTGTAGCCGACGTACG 740

RESULT 10
US-10-425-115-154424
; Sequence 154424, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 154424
; LENGTH: 935
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_72415C.1
US-10-425-115-154424

Query Match 5.4%; Score 33.8; DB 8; Length 935;
Best Local Similarity 52.5%; Pred. No. 4;
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 461 CAGGGACTATTCCGACCGACCTCAACCTGGTGTGTCATGACGACAAATCTCGTATTG 520
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 593 CTGGGCATATGACCGGAGTCAAGCCCAAGGAGTCCAAACGATGTTTAGGAAATGGG 652
QY 521 ATATGCCGGATTTTATGACATATGGTCAAGTCCGGCAGCATTTACTCACTTGTGCTTCCA 580
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 653 TTTCACGGGATCCTCTCTGATATTACGTGCTCTGAGAGAATTACGTACGTGCTGCTCCTA 712
QY 581 TGGGTTTCTTCGGGTACAGT 601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 713 TGAGTGTAGCCGACGTACG 733

RESULT 11
US-09-925-065A-41609
; Sequence 41609, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
```

Query Match 5.4%; Score 33.4; DB 9; Length 706;
Best Local Similarity 47.4%; Pred. No. 4.7;
Matches 100; Conservative 0; Mismatches 111; Indels

| | | | |
|-----|----|---|------|
| 434 | Qy | CTGCTGAGATATATGCAAAATTCAGGACCTTACCCCTGGTG | 493 |
| 910 | Db | CTGCGGATGTGAATGTGAATGAATACCCAGCAAGTTTACAGCCAAAGTG | 969 |
| 494 | Qy | TGTCATGACGACCAAAATCTCGTATTTGATATGCCGGAATTTTATGACATATGTCGA | 548 |
| 970 | Db | TGATGTTTGAATATGAATCAAGTGTTTCAATATGCCGCTAGTATGACAAATGTTAA | 1024 |

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; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 427028
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-427028
```

```
Query Match      5.3%; Score 33.2; DB 4; Length 534;
Best Local Similarity 52.2%; Pred. No. 4.7;
Matches 71; Conservative 1; Mismatches 64; Indels 0; Gaps 0;

QY 253 AGAGTTAACTCCCTGCGAGGAGTTAAGAGTGTGGGGTACGACGGGATAGGTGAAACCGCA 312
Db 191 ACATTTAACAGGCTGCAAGAGTTGCTCTCTCCCAATGGGGTAGGTCAGGACT 132
QY 313 AATGGTGGTTTTGGGTTATCAACATCACCATAAGAAATGACGGATCCACTCTCTATGGAG 372
Db 131 CACAGAGAGTCAGGGCTTTTCATCATTAACAGAGTAAAGAGCCATTACCCCCCATGGTG 72
QY 373 GTCGTTGATGGCATAT 388
Db 71 CCTGTGGTGGCCATGT 56
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RESULT 15

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US-09-925-065A-178736/c
; Sequence 178736, Application US/09925065A
; Publication No. US2005028172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178736
; LENGTH: 641
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-178736
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```
Query Match      5.3%; Score 32.8; DB 4; Length 641;
Best Local Similarity 55.2%; Pred. No. 7.1;
Matches 64; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 176 CTACGACTTCATCTTCTCAGTCGAAGTTACGATATATCCCGTTTCACACATACGGGAGG 235
Db 618 CTTTGTCTTCATTTTAAATATAAATAAAGTATACATCTGTTTCCCTTTGCTTCTTGG 559
QY 236 TAGGAGACTTGGAAATTAGATTAACTCCCTGCGAGCAAGTTAAGAGTGTGGGTAC 291
Db 558 TATAGCGCTGTAACCTTACATAACTTTCCCGACCATTCAGTTTAAAGCTGTGGATAC 503
```

Search completed: April 12, 2006, 08:11:40
Job time : 800 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2006, 07:59:29 ; Search time 670 Seconds
(without alignments)
3733.258 Million cell updates/sec

Title: US-10-784-592-18_COPY_124_744

Perfect score: 621

Sequence: 1 aaacggtgatgatgctg.....aaacgacgatgctcttcg 621

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters: 18562198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:*

- 1: /SIDSS/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /SIDSS/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /SIDSS/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 7: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 8: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 9: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 10: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 11: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 12: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 13: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 14: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 15: /SIDSS/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-----------------------|
| C 1 | 34.2 | 5.5 | 1502 | 6 | US-09-925-065A-724617 |
| C 2 | 33.8 | 5.4 | 591 | 6 | US-09-925-065A-867215 |
| C 3 | 33.8 | 5.4 | 1240 | 6 | US-09-925-065A-41609 |
| C 4 | 33.8 | 5.4 | 1240 | 9 | US-10-301-480-142847 |
| C 5 | 33.8 | 5.4 | 1240 | 10 | US-10-301-480-142847 |
| C 6 | 33.2 | 5.3 | 534 | 6 | US-09-925-065A-427028 |
| C 7 | 33.2 | 5.3 | 534 | 10 | US-10-301-480-490436 |
| C 8 | 33.2 | 5.3 | 534 | 10 | US-10-301-480-1103845 |
| C 9 | 32.8 | 5.3 | 641 | 6 | US-09-925-065A-178736 |
| C 10 | 32.8 | 5.3 | 650 | 10 | US-10-301-480-269706 |
| C 11 | 32.8 | 5.3 | 650 | 10 | US-10-301-480-883115 |
| C 12 | 32.6 | 5.2 | 566 | 6 | US-09-925-065A-604703 |
| C 13 | 32.6 | 5.2 | 566 | 6 | US-09-925-065A-604704 |
| C 14 | 32.4 | 5.2 | 611 | 6 | US-09-925-065A-760902 |
| C 15 | 32.2 | 5.2 | 598 | 6 | US-09-925-065A-301137 |
| C 16 | 31.8 | 5.1 | 533 | 6 | US-09-925-065A-413580 |
| C 17 | 31.8 | 5.1 | 551 | 10 | US-10-301-480-479582 |
| C 18 | 31.8 | 5.1 | 551 | 10 | US-10-301-480-1092991 |

| | | | | | | |
|------|------|-----|-------|----|-----------------------|--------------------|
| C 19 | 31.8 | 5.1 | 557 | 10 | US-10-301-480-492045 | Sequence 492045, |
| C 20 | 31.8 | 5.1 | 557 | 10 | US-10-301-480-1105454 | Sequence 1105454, |
| C 21 | 31.8 | 5.1 | 573 | 6 | US-09-925-065A-429103 | Sequence 429103, |
| C 22 | 31.6 | 5.1 | 615 | 6 | US-09-925-065A-517010 | Sequence 517010, |
| C 23 | 31.6 | 5.1 | 1394 | 6 | US-09-925-065A-711186 | Sequence 711186, |
| C 24 | 31.4 | 5.1 | 540 | 6 | US-09-925-065A-747461 | Sequence 747461, |
| C 25 | 31.4 | 5.1 | 545 | 6 | US-09-925-065A-746148 | Sequence 746148, |
| C 26 | 31.4 | 5.1 | 611 | 6 | US-09-925-065A-226317 | Sequence 226317, |
| C 27 | 31.4 | 5.1 | 1848 | 8 | US-10-467-857-1219 | Sequence 1219, Ap |
| C 28 | 31.2 | 5.0 | 505 | 10 | US-10-301-480-471976 | Sequence 471976, |
| C 29 | 31.2 | 5.0 | 505 | 10 | US-10-301-480-1085385 | Sequence 1085385, |
| C 30 | 31.2 | 5.0 | 524 | 6 | US-09-925-065A-405101 | Sequence 405101, |
| C 31 | 31.2 | 5.0 | 1173 | 8 | US-10-517-939-27 | Sequence 27, Appl |
| C 32 | 31.2 | 5.0 | 1715 | 11 | US-11-096-568A-5015 | Sequence 5015, App |
| C 33 | 31 | 5.0 | 23246 | 9 | US-10-330-773-567 | Sequence 567, App |
| C 34 | 30.8 | 5.0 | 505 | 10 | US-10-301-480-1085384 | Sequence 1085384, |
| C 35 | 30.8 | 5.0 | 524 | 6 | US-09-925-065A-405100 | Sequence 405100, |
| C 36 | 30.8 | 5.0 | 571 | 6 | US-09-925-065A-488015 | Sequence 488015, |
| C 37 | 30.8 | 5.0 | 641 | 6 | US-09-925-065A-772763 | Sequence 772763, |
| C 38 | 30.8 | 5.0 | 648 | 6 | US-09-925-065A-768565 | Sequence 768565, |
| C 39 | 30.8 | 5.0 | 846 | 6 | US-09-925-065A-94388 | Sequence 94388, A |
| C 40 | 30.8 | 5.0 | 846 | 9 | US-10-301-480-195630 | Sequence 195630, |
| C 41 | 30.8 | 5.0 | 846 | 10 | US-10-301-480-809039 | Sequence 809039, |
| C 42 | 30.8 | 5.0 | 1995 | 8 | US-10-793-626-1257 | Sequence 1257, Ap |
| C 43 | 30.8 | 5.0 | 3356 | 8 | US-10-793-626-3920 | Sequence 3920, Ap |
| C 44 | 30.6 | 4.9 | 507 | 6 | US-09-925-065A-512361 | Sequence 512361, |
| C 45 | 30.6 | 4.9 | 622 | 6 | US-09-925-065A-733858 | Sequence 733858, |

ALIGNMENTS

RESULT 1

US-09-925-065A-724617/c
; Sequence 724617, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 724617
; LENGTH: 1502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-724617

Query Match 5.5%; Score 34.2; DB 6; Length 1502;
Best Local Similarity 45.6%; Pred. No. 3.4;
Matches 120; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 197 | CGAGTTACGATATATCCCGTTTCACATACCGGAGGTAGGAGCTTGGAATTTAGAG | 256 |
| Db | 783 | CTAATGTAGGAGCATTTCTGCGATGCTCAAGACACGAAAGCCCTGTGTGATAGAG | 724 |
| Qy | 257 | TTAACCTCCCTGCAGCAAGTTAAGAGTGTGGGGTACGACGGGATAGGTGAAACCGCAATG | 316 |
| Db | 723 | TGAAGTGGATGGTTGTGAAGGAAGTAGTATATATGTTGAAGAGATGAACAGGAGGTC | 664 |


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US-10-301-480-756256
; Sequence 756256, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 756256
; LENGTH: 1240
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-756256

Query Match          5.4%; Score 33.8; DB 10; Length 1240;
Best Local Similarity 51.0%; Pred. No. 4.3;
Matches 80; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy 361 ACTCTATGGAGGTCGTTGATGGCATATTCATTTGCAGAACTTAAACGGGAACGTTTAT 420
Db 145 ACTCTTTTACCTCAGCATGCTACTGTTTCTGATGACCAAGATAAAACTGAACTTTAAA 204
Qy 421 CAGCGGATTTCTACTGCTGATATATGCAATATCAAAATTCAGGACTATTCGACCGAC 480
Db 205 AATCTCTCTTCACTGTTGTATATATATAAAAAAATAATCTGACCTTTATCACCAAA 264
Qy 481 CTCAACCTGCTGTGTCATGACGACAAATCTCTAT 517
Db 265 GTCAACAATCCAGTGAAGAGTGTCAATCAGGAAT 301

RESULT 6
US-09-925-065A-427028/c
; Sequence 427028, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 427028
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-427028

Query Match          5.3%; Score 33.2; DB 6; Length 534;
Best Local Similarity 52.2%; Pred. No. 4.7;
Matches 71; Conservative 1; Mismatches 64; Indels 0; Gaps 0;

Qy 253 AGAGTTAACTCCCTGCAGCAAGTTAAGAGTGTGGGGTACGACGGGATAGGTGAACCGCA 312
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Db 191 ACATTTAACAGGCTGCAAGAGTTGCTCTCTCTCCCACTGCTGGGTAGGTGAGACT 132
Qy 313 AATGGTGCCTTTTGGGTTATCAACATCACCATAAGAAATGACGGATCCACTCTTATGGAG 372
Db 131 CACAGAGAGTCAGGCTTTTTCATCATTTACACAGAGTAAAGAGCCATTTCACCCCCATGGTG 72
Qy 373 GTCGTTGATGGCATAT 388
Db 71 CCTGTGTGGGCCATGT 56

RESULT 7
US-10-301-480-490436/c
; Sequence 490436, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 490436
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-490436

Query Match          5.3%; Score 33.2; DB 10; Length 534;
Best Local Similarity 52.2%; Pred. No. 4.7;
Matches 71; Conservative 1; Mismatches 64; Indels 0; Gaps 0;

Qy 253 AGAGTTAACTCCCTGCAGCAAGTTAAGAGTGTGGGGTACGACGGGATAGGTGAACCGCA 312
Db 191 ACATTTAACAGGCTGCAAGAGTTGCTCTCTCTCCCACTGCTGGGTAGGTGAGACT 132
Qy 313 AATGGTGCCTTTTGGGTTATCAACATCACCATAAGAAATGACGGATCCACTCTTATGGAG 372
Db 131 CACAGAGAGTCAGGCTTTTTCATCATTTACACAGAGTAAAGAGCCATTTCACCCCCATGGTG 72
Qy 373 GTCGTTGATGGCATAT 388
Db 71 CCTGTGTGGGCCATGT 56

RESULT 8
US-10-301-480-1103845/c
; Sequence 1103845, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1103845
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapien
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; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 604703
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-604703

Query Match      5.2%; Score 32.6; DB 6; Length 566;
Best Local Similarity 55.9%; Pred. No. 7.5;
Matches 62; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 151 TTGCAACATGCGCAACATCAAGCTGCTACGACTTCTCAGTCGAACTTACGATAT 210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 90 TTGTTACATCAGCAACTAGGAACTAATGCACATTCCTGTTTTCAGAGGGTCTTGAAG 149

Qy 211 ATCCGGTTTACACATACGGAAGGTAGGACTTGGAAATAGAGTTAAC 261
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 150 TTCTGTTGAACACTTGCACACACTTGGTAGTCTCGGTGTTTCATTTAAC 200

RESULT 13
US-09-925-065A-604704
; Sequence 604704, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 604704
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-604704

Query Match      5.2%; Score 32.6; DB 6; Length 566;
Best Local Similarity 55.9%; Pred. No. 7.5;
Matches 62; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 151 TTGCAACATGCGCAACATCAAGCTGCTACGACTTCTCAGTCGAACTTACGATAT 210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 90 TTGTTACATCAGCAACTAGGAACTAATGCACATTCCTGTTTTCAGAGGGTCTTGAAG 149

Qy 211 ATCCGGTTTACACATACGGAAGGTAGGACTTGGAAATAGAGTTAAC 261
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 150 TTCTGTTGAACACTTGCACACACTTGGTAGTCTCGGTGTTTCATTTAAC 200

RESULT 14
US-09-925-065A-760902/c
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; Sequence 760902, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 760902
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-760902

Query Match      5.2%; Score 32.4; DB 6; Length 611;
Best Local Similarity 52.2%; Pred. No. 8.9;
Matches 72; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 30 ACCCGGAACGCATCAACGGTAAGCGCTACAACTTCTTTGGTTAATTCGAGATAGTTC 89
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 291 ACCCAAGACCTGTTTACACTGTATCTCTCTCTCCATGGGTTAATCCCCAATTAGAGT 232

Qy 90 ACAGGTAGCAAGCAAGCAAGCAAACTCGAGTACGTCTCCGCTCATAGTCTACGAACTC 149
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 231 TTAGTAAGGAGCTAAGATTGCGATCTTGGCATCAGTCACTTACAGATCTGATGAAATC 172

Qy 150 ATTGCAACATCGCGCAACA 167
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 171 AGTGCCACATTCCTCTATA 154

RESULT 15
US-09-925-065A-301137
; Sequence 301137, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 301137
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-301137
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Query Match      5.2%; Score 32.2; DB 6; Length 598;
Best Local Similarity 49.7%; Pred. No. 10;
Matches 82; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 160 GCGCAACATCAAGCTGCTAGGACTTCTCTCAGTCGAAGTTACGATATATCCCGTTT 219
Db 382 GGGACAGATGATGGTGTCTCTACTCAACTATGGCAGACGCGAGTGGGGCTAGTTAGGAAAG 441

Qy 220 CACACATACGGGAAGGTAGGAGACTTGGAAATTAGAGTTAACTCCCTGCAGCAAGTTAAG 279
Db 442 GGCACGTTCAAGAATGTACGACAATTGATATCAAGGGTTAGATAGAAAGAGGAGATAAAG 501

Qy 280 AGTGTGGGGTACGACGGGATAGGTGAACCGCAATGGTGGTTT 324
Db 502 ACGGGGCTGGTTTCTTGGCATGAGTACTGAGTAATTGTGTGTT 546

```

Search completed: April 12, 2006, 08:18:46
Job time : 672 secs